GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein search, using sw model
                                                                                                                              SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-867-753-2
986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       April 27, 2003, 19:37:10; Search time 69 Seconds (without alignments) 549.459 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                            671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MARSLVHDTVFYCLSVYQVK.....LMLANELRADPDDCVYIVVD 184
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                             sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                                sp_invertebrate:*
                                                                                                                                                 sp_organelle:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16	15	14	13	12	11	10	9	8	7	0	U	4	ω	2	-	Result No.
186	187	188	188.5	190	191.5	191.5	196	197	197	212	212.5	216	216	260.5	789	Score
18.9	19.0	19.1	19.1	19.3	19.4	19.4	19.9	20.0	20.0	21.5	21.6	21.9	21.9	26.4	80.0	Query Match L
563	328	227	371	640	562	248	314	387	382	286	227	288	288	137	148	Length DB
5	13	11	\$	Çī	4	13	11	11	11	σ	11	4	4	4	4	Ď
Q9VTX6	Q9W7M5	070238	061282	Q8T0M4	Q96QS3	012952	054817	Q9Z2U3	088933	Q8T6I5	Q9EQM5	Q9BQY4	Q9BR00	Q9Y4W1	095030	ID
Q9vtx6 drosophila	Q9w7m5 brachydanio	O70238 mus musculu	061282 hemicentrot	Q8t0m4 drosophila	Q96qs3 homo sapien	Ol2952 cynops pyrr	O54817 mus musculu	Q9z2u3 mus musculu	O88933 mus musculu	Q8t6i5 branchiosto	Q9eqm5 mus musculu	•	homo	Q9y4w1 homo sapien	095030 homo sapien	Description

45 173 17.5 210 11 Q9QYR0	44 174 17.6 464 5 Q9NDA9	17.6 295 5	174 17.6	41 174.5 17.7 350 13 Q9IAL2	175 17.7 484	371 5 0	υ -	835 4	_	5	17.8 479 13	17.8 479	176 17.8 370 5 Q	w	176.5 17.9 493 11	177 18.0 387 13	177.5 18.0	179 18.2	179 18.2	179 18.2	179.5 18.2 362 5 Q	180 18.3	180 18.3 299 11	180 18.3	180 18.3	181 18.4 365 6 Q	18 182.5 18.5 185 13 P79857
Q9qyr0 stochomys 1	Q9nda9 branchiosto	Q968z4 hemicentrot	073678 oryzias lat		mus mu	046169 tribolium c		Q96h85 homo sapien	Q26441 drosophila		013081 coturnix co	Q9cxi6 mus musculu	Q25411 lineus sang	Q8uvd3 gallus gall	mus mu	093582 gallus gall	Q98tg7 gallus gall	Q9bi30 ciona intes	Q8t8c1 gryllus bim	046170 tribolium c	Q21836 caenorhabdi	Q9jlt8 rattus norv	. Q9wtq9 rattus norv	Q8sq03 canis famil	Q8r4i3 mus musculu	Q9gma3 bos taurus	P79857 pleurodeles

## ALIGNMENTS

Db Db	Qu Ma	2	S	Ę	DR	DR S	7 5	7 5	D R	RL	RA	RP	RN	RL	RT	RA	RP	RN	õ	8	ဂ္ဂ	SO	GN	DE	DT	DŢ	D.	AC	ID	RESULT 095030
1 MARSLVHDTVFYCLSVYQVKISPTPQLGAASSAEGHVGQGAPGLMGNNNPEGGVNHENGM 60 	Ouery Match 80.0%; Score 789; DB 4; Length 148; Best Local Similarity 100.0%; Pred. No. 6.3e-63; Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		F 148 AA:	NON TER 148 148	PROSITE; PS50071; HOMEOBOX_2; 1.	SMART; SM00389; HOX; 1.	THICHIELD TENOCOLOGY TOWNSON	Tribordro. Todo Circuit.	EMBL; AC005023; AAC78617.1;	Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.	Waterston R.;	SEQUENCE FROM N.A.	. [2]	Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.	"The sequence of Homo sapiens BAC clone GS1-42113.";	Leonard S., Graves T., Cofman M.;	SEQUENCE FROM N.A.	[1]		Primates; Catarrhin	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).		protein (	(TrEMBLrel. 19,	(TrEMBLrel. 10,	1999	••	O95030 PRELIMINARY; PRT; 148 AA.	11 1 30 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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Best Local :
                                                                                                                                                                                                                                                   Q9BR00;
01-JUN-2001
01-JUN-2001
01-MAR-2002
                                                                                                                                                  Hypothetical 31.6 kDa protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9Y4W1;
                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                     Q9BR00
SEQUENCE FROM N.A. Howell G.R., Huckl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
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EMBL; AL049631; CAB46720.1;
HSSP; P06601; 1FJL
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Homo sapiens (Human).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ513M9.1 (Novel homeobox domain protein) (Fragment).
                                                                                           NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00028; POUDOMAIN. ProDom; PD000010; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0024; HOMEOBOX PRINTS; PRO0031; HTHREPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000047; HTH_repress
InterPro; IPR000327; POU_domain.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bird
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DJ513M9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPEQQQEEPPLLELKQEQEEPPQTTVEGPQPAEGPQTAEGPQPPERKRRRRTAFTQFQLQ 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFRHTQYPDVPTRRELAENLGVTEDKVR 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137
137 AA;
                                                                                                                                                                                                                                                   (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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   Huckle
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16126 MW;
   Ε.
                                                                                                                              Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.4%;
47.5%;
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Pred. No. 7.9
   M.T.;
                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9B2E9CF358E59ABC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                     288
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                                                                                                                              Hominidae;
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                                                                                                                                                                                                                                                       update)
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                                                                                                                                                        Euteleostomi;
                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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RESULT 4 .
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Best Local
                                                                                                                                                                                                Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama J. Kawakami B., Nagai K., Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 31.7 kDa protein (CDNA FLJ25396 fis, c
(Homeobox protein) (Homeobox protein from AL590526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodom; PD000010; Homeobox; 1.
SMART; SM0389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00011; HOMEOBOX_2; 1.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
                                                               Yin Y., Jin Y., Levine A.J.;
"Molecular cloning and characterization of a novel testis homeobox gene, THG1, as a potential testicular tumor suppressor gene.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                      Kawakami B., Nagai K., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BQY4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BQY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: N
EMBL; AL590524; CAC36517.1;
HSSP; P06601; 1FJL.
             Strausberg R.;
                           SEQUENCE FROM N.A. TISSUE=TESTIS;
                                                                                                                              SEQUENCE FROM N.A.
TISSUE=TESTIS;
                                                                                                                                                                                                                                                                                       TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Howell G.R., Huckl
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   THG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-binding; Homeobox; Hypothetical protein; Nuclear psequence 288 AA; 31637 MW; 50B571B13DB712B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001356; Homeobox.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                         Ishibashi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157
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R
(JAN-2002)
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                                                                                                                                                                                                                                                                         Kanehori K., Yosida M., Watanabe
                                                                                                                                                                                                                                                                                                                                                E.,
                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
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the EMBL/GenBank/DDBJ
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Pred. No. 1.7e
23; Mismatches
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EMBL/GenBank/DDBJ
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.7e-11;
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databases
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Best Local
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Best Local
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Q9EQM5;
01-MAR-2001
                                                                                                                                                                                                                                                                                    ProDom; PD000010; Homeobox; 1.

SMART; SM00389; HOX; 1.

PROSITE; PS50071; HOMEOBOX_2; 1.

SEQUENCE 227 AA; 25112 MW; D39CF6795AF682DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS00215; MITOCH_CARRIER;
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AL590526; CAC36519.1; -.
EMBL; AK058125; BAB71675.1; -.
EMBL; AK058125; BAB71675.1; -.
EMBL; BC0217219; AAL02160.1; -.
EMBL; BC021719; AAH21719.1; -.
HSSP; P06601; 1FJL;
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001356; Homeob
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF201698; AAG36768.1; -. MGD; MGI:1925663; 1600026001Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takasaki N., McIsaac R., Dean J.;
"Gpbox, a novel homeobox gene preferentially expressed in cells at the onset of sexual dimorphism in mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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01-MAR-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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       114
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DNIQEEGGENIDQQPPQQEAAIPE----GMRNPQAGNYLAHQRTRRTRFTHSQLRDLER
                                                                                                                                                   GAASSAEGHVGQGAPGLMGNMNP-----EGGVNHENGMNRDGGM----
                               --IPEGGGGN--QEPRQQPQPPPEEPAQAAMEGPQPEN--MQPRTRRTKFTLLQVEELES 120
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                                                                                                    GGLDQGEGAQGEVAGGEQAQEEPAPLSPAQEATGGEEEGENKEGEMEGRHAGDGASGPED
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34.9%; Pro
ative 23;
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bx; Hypothetical protein; Nuclear 131691 MW; 280E007064515808
                                                                                                                                                                                                    21.6%; Score 212.5; 35.7%; Pred. No. 2.76 tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Homeobox.
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20,
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Last sequence update)
Last annotation update)
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Pred. No. 1.7e-11;
3; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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088933;
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jackman W.R. Jr., Kimmel C.B.;
"Coincident iterated gene expression in the amphioxus neural submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF465939; AALB3210.1; -.
Homeobox; DNA-binding; Nuclear protein.
SEQUENCE 286 AA; 31551 MW; 6BF50B62D92958C1 CRC64;
         SEQUENCE FROM N.A.
MEDLINE=97392770; PubMed=9245514;
Li Y., Lemaire P., Behringer R.R.;
"Esx1, a novel X chromosome-linked homeobox gene extraembryonic tissues and male germ cells.";
                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                       MEDILINE-973-98449; PubMed-9256347;
MEDILINE-973-98449; PubMed-9256347;
Branford W.W., Zhao G.O., Valerius M.T., Weinste Birkenmeier E.H., Rowe L.B., Potter S.S.;
"Spx1, a novel X-linked homeobox gene expressed"
                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XOHS
                                                                                               "Spx1, a novel x-linked spermatogenesis.";
                                                                                                                                                                                                                                      ESX1 OR EPX.
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01-JUN-2002
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                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                Homeobox protein
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                                                                                    Mech. Dev. 65:87-98(1997).
                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                     142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity 32.9
52; Conservative
188:85-95(1997).
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tazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                 SPX1.
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. 21, Last sequer
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n transcription /
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08,
21,
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Inscription factor Shox.
                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                       Created)
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Pred. No. 3.9e-11;
4; Mismatches 48
                                                                                                                                                                                               Sciurognathi;
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                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                             Craniata;
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                                                                                                                                     Weinstein
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                       expressed
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                                                                                                                                                                                                Murinae;
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                       in mouse
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SQUERRY DESCRIPTION OF SQUERRY STREET STREET
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Best Local Similarity
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MGD; MGI:1096388; Esx1.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_repressr.
Pfam; PF00046; homeobox; 1.
PRINTS; PR00031; HTHEPRESSR.
PRODOM; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9Z2U3;
Q9Z2U3;
01-MAY-1999
HSSP; P06601; 1FJL.
MGD; MGI:1096388; Esx1.
InterPro; IPR001356; Ho
InterPro; IPR000047; HT
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE FROM N.A.
Branford W.W., Pot
                                                                                     Activity of the ESX1 Homeoprotein.";
Mol. Cell. Biol. 20:661-671(2000).
-i- SUBCELLULAR LOCATION: NUCLEAR (BEMBL; AF017734; AAD01621.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Branford W.W., Potter Submitted (AUG-1998) t
                                                                                                                                                                                                                          MEDLINE=20079279; PubMed=10611245;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-129,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                              Yan Y.T., Stein S.M., Ding J., Shen M.
"A Novel PF/PN Motif Inhibits Nuclear
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                           ESX1 OR EPX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abate-Shen C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LMQPVAQSSPQPLPANPLQAPQQPEEQEEEEEEEQPGEEQPQQE-PKPRRYRICFTPIQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -MIPEGGGGNQ----EPRQQPQPP----PEEPAQAAMEGPQPENMQPRTRRTKFTLLQVE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQVKISPTPQLGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGG------
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AF017735;
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                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 10, Last sequence update) (TrEMBLrel. 21, Last annotation update) protein EPX (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J., Sciavolino P.J., Wang H., Shen M.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD01622.1; -
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                                                                                                                                                                                                                                                                                                                                      Chordata;
Rođentia;
  Homeobox.
HTH_repressr
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the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
EC92301A84DA6175
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                                                                                                              SIMILARITY)
                                                                                                                                                                                 .M., Abate-Shen Localization a
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1.2e-09;
72;
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                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
; Murinae; Mus
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                                                      Matches
                                                                    Query Match
Best Local
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Best Local :
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01-JUN-1998
01-MAR-2002
Paired-like
                                                                                                                                                                                                                                                                                                                                 **ETKALP=www.ss, pubMed=9245514;
MEDLINE=97392770; PubMed=9245514;
Li Y., Lemaire P., Behringer R.R.;
"Esx1, a novel X chromosome-linked homeobox gene expressed "Esx1, a novel X chromosome-linked homeobox gene expressed"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000010; Homeo SMART; SM00389; HOX; 1
                                                                                                                                                                                                        TRANSFAC; T03474; -.
MGD; MGI:1096388; Esx1.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTM_repressr
Pfam; PF00046; homeobox; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00031; HTHREPRESSR. PRINTS; PR01217; PRICHEXTENSN
                                                                                                           PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear pSEQUENCE 314 AA; 35969 MW; 7
                                                                                                                                                                  ProDom; PD000010; Homeobox; 1. SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                       Dev. Biol. 188:85-95(1997).
-!- SUBCELLULAR LOCATION: NUCLEAR
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Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                           PRINTS; PR00031; HTHREPRESSR.
                                                                                                                                                                                                                                                                                         EMBL; AF004211; AAB94670.1;
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SWISS;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESX1 OR ETX.
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                                                                                                                                                                                                                                                                             HSSP; P06601; 1FJL.
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 16
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                           YQVKISPTPQLGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGG---
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YQEPEGFEPSRGEAAAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMQPVAQSSPQPLPANPLQAPQQPEEQEEEEEEEQPGEEQPQQE-PKPRRYRICFTPIQLQ
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                                                      . Similarity 59; Conserv
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                                                                   19.9%;
34.1%;
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n containing protein.
-VAEAPQAWNGNENLGGGFLEANAQLGEADAAPVRQSLMRP
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Last annotation update)
                                                     Score 196; DB 11;
Pred. No. 1.2e-09;
8; Mismatches 72;
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Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                           protein.
72568F81DA4AA246 CRC64;
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01-JUL-1997
01-NOV-1998
01-MAR-2002
  Q96QS3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 248 AA; 27687 MW; 98BDBA7D61DB59D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000010; Homeobox; 1. SMART; SM00389; HOX; 1.
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Biochem. Biophys. Res. Commun. 218:395-401(1996).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AB001938; BAA24005.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96136334; PubMed-8573168; Takabatake T., Takahashi T.C., In Takabation of two Cynops genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sone K., Takeshima K., Takahashi T., Dev. Genes Evol. 207:147-155(1997).
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                                                                                                                                                                                                                                                                     --RTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRH 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YQVKISPTPQLGA-ASSAEGHVG------QGAPGLMGNMNPEGGVNHENGMNRDG 64
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                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                          -YDGSSSVLMSPMPHQMMPYMNVGTLSRSELQLLNQLHCR 151
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s, fork head and
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Best Local
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01-JUN-2002
01-JUN-2002
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa Y. C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY069177; AAL39322.1; -
                                                                                               STRAIN-BERKELEY;
Stapleton
                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                             Q8T0M4;
                                                                                                                                                                                                                          TOE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohira R.H., Zhang Y.H., Guo W., Dipple K., Shih S., Doerr J Huang B.-L., Fu L., Abu-Khalil A., Geschwind D., McCabe E.; "Human ARX gene: genomic characterization and expression."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AY038071; AAK93901.1; -. IRROJ3554; Homeobox. InterPro; IPR003554; Homeo_OAR.

Pfam; PF00046; homeobox; 1.
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                                                                                                                                                     NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; PROSITE; PS50071;
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                                                                                                                                                                                                                                                                                                                                                                                            TLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGTGTEDDEEEELLEDEEEEELLEDDEEEELLEDDARALLKEPRRCPVAATGAVAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGN--
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Last annotation update)
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Pred. No. 5.8
                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FBDF41E387C65532 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                           640
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                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                 Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 562;
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                                                      ge R.,
C.J.,
Wan K.,
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Query Match

19.3%;

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Best Local
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                      DNA-binding; home 371 AA;
                                                                                                                                                                                                                             PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS0071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear ps
SEQUENCE 371 AA; 41272 MW; 61
                                                                                                                                                                                                                                                                                                                                                                                    "Two isoforms of orthodenticle-related proteins (Henhancer element of sea urchin arylsulfatase gene. Dev. Biol. 181:284-295(1997).

-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           061282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-97166044; PubMed-9013937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Orthodenticle-related protein.
                                                                                                                                                                                                                                                                                       SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                  PRINTS; PR00024; HOMEOBOX. ProDom; PD000010; Homeobox.
                                                                                                                                                                                                                                                                                                                              Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                          EMBL; AB011526; BAA28675.1; HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sakamoto N., Akasaka K., Mitsunaga-Nakatsubo K., Takata
Nishitani T., Shimada H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimada H., Akasaka K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Echinoidea; Euechinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hemicentrotus pulcherrimus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113
    133
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                                                                                                                 25
                                                                                                                                          14 LSVYQVKISPTPQLGAASSAE-----GHVGQGAPGLMGNMNPEGGVN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQR 163
RERTTFTRAQLDVLETLFSRTRYPDIFMREEVAMKINLPESRVQVWFKNRRAKCRQQQQQ
                           TRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQRE 164
                                                         AYSNPMYGEGALPAPDRHVPP---TQQHPMFQPQVLGPMTSERPHSNGVDPPRKQ----R 132
                                                                                  -HENGMNRDGGM-----IPEGGGGNQEPRQQPQ----PPPEEPAQAAMEGPQPENMQPR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQLDELEKEFDKSHYPCVNTREKLAARTALSEARVQVWFSNRRAKWRRHQR 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGRLSLPALSPDSGS-----RDSRSPDADANRMIDIEGEDSESQDSDQPKFRRNRTTFSP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------MIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPENM---QPRTR--RTKFTL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPPGGGPAGAGGALQPGGSGSSYGSDGNMSSNPNSSNSNTTHSNGHNTNSGSGCGDSSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPQLGAASSAEGHVGQGAPGLM----GNM--NP---EGGVNHENGMNRDGG------
                                                                                                               LNVKPMKLE---RVGMSSSPPRLTIDCGNTGRSP--VPSHMEPPGGARVPYPMHLYPYQY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 32.: 55; Conservative
                                                                                                                                                                                      Similarity
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                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                    Homeobox; 1.
                                                                                                                                                                                    19.1%;
28.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitsunaga-Nakatsubo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                       Score 188.5;
Pred. No. 6.
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                                                                                                                                                                                                                               protein.
6F4BEF71251E5EF7 CRC64;
                                                                                                                                                                        Mismatches
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ches 60;
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ies 53;
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                                                                                                                                                                       Indels
                                                                                                                                                                                                Length 371;
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                                                                                                                                                                       41;
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                                                                                                                                                                     Gaps
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Best Local
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070238;
01-AUG-1998
01-MAY-1999
01-MAR-2002
                                                                                                                                                                                                           Q9W7M5;
Brachydanio rerio (Zebrafish) (Zebra danio)
Eukaryota; Metazoa; Chordata; Craniata; Ver
Actinopterygii; Neopterygii; Teleostei; Ost;
                                                                                                                                                                       01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS50071; HOWEOBOX_2; 1.
SEQUENCE 227 AA; 25484 MW; 0FEF5EC1C5EAE374 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AOMeco...
PSX1.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                          "Isolation of the mRNA encoding
                                                                                      Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                  Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                                  OTP OR OTP
                                                                                                                                                           Orthopedia protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Han Y.J., Park A.R., Seong Submitted (JAN-1999) to the EMBL; AF017453; AAD08781.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "PSX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T03294; -.
MGD; MGI:1202888; Psx1.
InterPro; IPR001356; Homeobox.
                                  Danio rerio.";
                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Han Y.J., Park A.R.,
                                                                                                                                                                                                                                                                              169
                                                                                                                                                                                                                                                                                                                         114
                                                                                                                                                                                                                                                                                                  121 VFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQRELM
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                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , a novel murine homeobox gene expressed in 207:159-166(1998) .
                                                                                                                                                                                                                                                                            LFQETRYPSLRARRDLARWMGVDECDVQNWFRMRRALFQRNRRVLM
                                                                                                                                                                                                                                                                                                                         DSILEEGGENIDQQPPQQEAASPD-----SIRNPHVLNRLAQLRYRRTRFTHSQLHDLER 168
                                                                                                                                                                                                                                                                                                                                             --IPEGGGGN--QEPRQQPQPPPEEPAQAAMEGPQPEN--MQPRTRRTKFTLLQVEELES
                                                                                                                                                                                                                                                                                                                                                                    GEFDQGEGAQGEVAGGEQAQEEPAPLSPAQEATGGEEEGENKEGEMEGRHAGDGASSSED 113
                                                                                                                                                                                                                                                                                                                                                                                         GAASSAEGHVGQGAPGLMGNMNP-----EGGVNHENGMNRDGGM------
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55; Conser
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2 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=9511757;
R., Sung D.Y., Chun J.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                             19.1%; Score 188; DB 11; 33.1%; Pred. No. 4.2e-09; tive 22; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seong D.Y., Chun J.Y.; to the EMBL/GenBank/DDBJ databases.
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Sciurognathi; Muridae;
                                          Duga
Otp (
                                         (Orthopedia) in
                                                                                                                                                                                                                     328
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                                                                                                              Ostariophysi;
                                                                                                                          Vertebrata; Euteleostomi;
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                                                                                                              Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                       227;
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Search completed: April 28, 2003, 03:35:05 Job time: 74 secs
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R ZFIN, ZDB-GENE-990708-7; otp.
R InterPro; IPR001356; Homeobox.
R InterPro; IPR001356; Homeobox.
R InterPro; IPR000047; HTH_TepreSST.
R InterPro; IPR000047; HTH_TepreSST.
R Pfam; PF00046; homeobox: 1.
R PRINTS; PR00031; HTHREPRESSR.
R PRINTS; PR00031; HTHREPRESSR.
R PRODOM; PD00010; Homeobox; 1.
R PRODOM; PD00010; Homeobox; 1.
R PROSITE; PS00027; HOMEOBOX_1; 1.
R PROSITE; PS00027; HOMEOBOX_2; 1.
R PROSITE; PS00027; HOMEOBOX_2; 1.
R PROSITE; PS00027; HOMEOBOX_2; 1.
SEQUENCE 328 AA; 35488 MW; 7CCA8C489011C3EC CRC64;
                                                                                                                                                                                                                                                                                                                                          Ouery Match 19.0%; Score 187; DB 13; Length 328; Best Local Similarity 30.9%; Pred. No. 7.8e-09; Matches 56; Conservative 22; Mismatches 61; Indels 42; Gaps
                                                                   179 A 179
                                                                                                                                173 A 173
                                                                                                                                                                                                     78 GSN-PNGMQ-----QVNAKDQEKQQQ-----QNSNQTGGQQNQQKQKRHRTRFTP 121
                                                                                                                                                                                                                         32 AELLVHREALKC------RLGGTDS--GHPGDLTSATETVEGTTLLPGEEISNG 77
                                                                                                                                                                                                                                                                                                             2 ARSLYHDTVFYCLSVYQVKISPTPQLGAASSAEGHVG-----QGAPGLMGNMNPEG 52
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Result
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Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  174.5
173.5
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986
1 MARSLVHDTVFYCLSVYQVK......LMLANELRADPDDCVYIVVD
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   PIR_73:*
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A56570
                                                                             T24046
A55882
A45452
I49265
I51226
JC6540
JC6540
JC65130
S156130
S156130
S15623
A47539
JW0097
A26332
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S70617
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                                dene alx3 protein B gene alx3 protein paired box transcr paired box transcr homeotic protein g homeotic protein g homeotic protein g
                                                                                    reversed polarity homeotic protein g bicoid-related hom
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homeotic protein homeobox protein
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167.5 17.0 283 2 150112 168.5 16.9 284 2 \$60250 166.5 16.9 284 2 \$60251 166 16.8 314 2 \$52273 166 16.8 318 2 \$52424 166 16.8 319 2 \$718786 165 16.8 319 2 \$718786 165.5 16.8 319 2 \$72842 165.5 16.8 363 2 \$7750 165.5 16.8 363 2 \$7750 165.5 16.8 363 2 \$7750 165.5 16.7 398 2 \$20881 165 16.7 798 2 \$20881 165 16.7 398 2 \$20881 165 16.6 354 2 \$339406 163.5 16.6 355 2 \$33945
283 2 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 2 3 1 8 2 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 2 3 1 8 2 2 2 3 1 8 2 2 2 3 1 8 2 2 2 3 1 8 2 2 2 3 1 8 2 2 2 3 1 8 2 2 2 3 1 8 2 2 2 3 1 8 2 2 2 3 1 8 2 2 2 3 1 8 2 2 2 3 1 8 2 2 3 1 8 2 2 3 1 8 2 2 3 1 8 2 2 3 1 8 2 2 3 1 8 2 2 3 1 8 2 2 3 1 8 2 2 3 1 8 2 2 3 1 8 2 2 3 1 8 2 2 3 1 8 2 2 3 1 8 2 2 3 1 8 2 3 1 8 2 2 3 1 8 2 3 1 8 2 3 1 8 2 3 1 8 2 3 1 8 2 3 1 8 2 3 1 8 2 3 1 8 2 3 1 8 2 3 1 8 3 1 8 2 3 1 8 3
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## ALIGNMENTS

RESULT 2  RESULT 2  A54677  A54677  homeotic protein goosecoid [validated] - human  C; Species: Homo sapiens (man)  C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Sep-2000  C; Accession: A54677  R; Blum, M.; De Robertis, E.M.; Kojis, T.; Heinzmann, C.; Klisak, I.; Geissert, D.; Sp  Genomics 21, 388-393, 1994  A; Title: Molecular cloning of the human homeobox gene goosecoid (GSC) and mapping of	140 vPCy 103pp 103pp 200 GKKF 161 HQR 161 HQR	Query Match 19.2%; Score 189.5; DB 2; Length 399; Best Local Similarity 30.1%; Pred. No. 2.2e-07; Matches 55; Conservative 22; Mismatches 49; Indels 57; Gaps 7;  Qy 23 PTPQLGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGNQEPRQ 79	A; Release number: 0.0324; MOLD: 3000222; FMID: 3420233 A; Contents: Embryo A; Accession: JC6522 A; Molecule type: mRNA A; Residues: 1-399 <qua> A; Cross-references: GB: AF001465; NID: 92352265; PIDN: AAC39943.1; PID: 92352266 C; Comment: This protein belongs to the family of paired-type homeodomain proteins, it C; Genetics: A; Gene: Alx-4 C; Superfamily: homeotic protein Hox B3; homeobox homology C; Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation F; 203-259/Domain: homeobox homology <hox></hox></qua>	RESULT 1  JC6522  patred-type homeodomain protein, Alx-4 - mouse C;Species: Mus musculus (house mouse) C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 31-Mar-2000 C;Accession: JC6522 R;Qu, S: Li, L:, Wisdom, R. Gene 203, 217-223, 1997 A;Title: Alx-4: CDNA Cloning and characterization of a novel paired-type homeodomain

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N;Alternate names: homeotic protein K-2b
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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A;Map position: 14932.1-14932.1
C;Superfamily: homeotic protein goosecoid; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription ref;156-212/Domain: homeobox homology <HOX>
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A;Accession: A54677
A;Status: preliminary; not compared with conceptual transposed type: DNA
A;Molecule type: DNA
A;Residues: 1-252 <BLU>
C;Genetics:
A;Gene: GDB:GSC
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A;Title: Gastrulation in the mouse: the role of the homeobox gene A;Reference number: A42768; MUID:92315328; PMID:1352187
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: A42768
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                                                            homeobox protein
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A;Note: sequence extracted from NCBI backbone (NCBIP:108110)
C;Superfamily: homeotic protein goosecoid; homeobox homology
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Best Local :
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --RTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRH 161
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36.1%;
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Pred. No. 2.8e-07;
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Pred. No. 2.8e-07;
6; Mismatches 37
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  24 - Sep - 1999
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C; Keywords: alter
F; 95-151/Domain:
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R;Kern, M.J.; Argao, E.A.; Birkenmeier,
Genomics 19, 334-340, 1994
                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-245 <KER>
                                                                                                                                                                                                                                                  A; Reference number: A; Accession: S26076
                                                                                                                                                                                                                                                                    A; Title: A novel murine homeobox gene isolated by a tissue specific PCR cloning A; Reference number: S26076; MUID:93027261; PMID:1383943
                                                                                                                                                                                                                                                                                                                                   C; Accession: S26076
R; Kern, M.J.; Witte
                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1999
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A; Residues: 1-217 <KER>
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A;Reference number: S260
A;Accession: S26077
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Nucleic Acids Res. 20, 5189-5195, 1992
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A; Residues: 1-217 < RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-217 < RES>
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                                                                                                                                                      A; Experimental source: fetal heart
                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 20, 5189-5195, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                        homeotic protein K-2a -
                                                                                                          Superfamily: unassigned homeobox proteins; homeobox homology; Reywords: alternative splicing; DNA binding; homeobox; nucle
                                           Query Match
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                       Local
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    L Similarity
49; Conser
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    Conservative
                                                                                          homeobox homology
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                       18.7%;
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29.0%; Pred. No. 2.86
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27;
                       Score 184.5;
Pred. No. 3.
                                                                                          <XOH>
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                                                                                                                                                                                                                                                                                                                                       Aronow,
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                       2e-07;
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                                                                                                                                                                                                                                                                                                                                       в.J.;
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ter, S.S.
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RESULT 7
S70617
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                                                                                                                                                                                                                                                                              A; Title: Drosophila goosecoid participates A; Reference number: S70617; MUID: 96272167; A; Accession: S70617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Schneitz, K.; Spielmann, P.; Noll, Genes Dev. 7, 114-129, 1993
A:Title: Molecular genetics of arist A; Reference number: A46403; MUID:931
A; Accession: A46403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
A46403
                                                             C; Function:
                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-419 <HAH>
                                                                                                                                                                                                                                                                                                                                                       R; Hahn, M.; Jaeckle, H.
EMBO J. 15, 3077-3084,
                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revi
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A; Residues: 1-384 <SCH>
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                                                                                     A; Map position:
                                                                                                            A; Cross-references:
                                                                                                                                A; Gene: gsc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AENLGVTEDKVRVWFKNKRARCRRHQR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTNSPVSDGNSDCEADEYAPK---RKQRRYRTTFTSFQLEELEKAFSRTHYPDVFTREEL
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                                                                                                            FlyBase:FBgn0010323
                                                                                                                                                                                                                                                                                                                                                                                                                                 #sequence_revision 10-Sep-1999
     a role in neurogenesis in post-gastrula for gastrulation like Xenopus goosecoid;
                                                                                                                                                                                                                                                                                                                                                            1996
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                                                                                                                                                                                  NID: g1399586;
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Pred. No. 6.8e-07;
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                                                                                                                                                                                  PIDN:AAB17948.1;
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A;Molecule type: mRNA
A;Residues: 1-185 <THO>
A;Cross-references: EMBL:X80040; NID:g510536;
R;Thomas, P.Q.; Rathjen, P.D.
Nucleic Acids Res. 20, 5840, 1992
                                                                                                                           R;Thomas, P.Q.; Johnson, B.V.; Rathjen, J.; Rathjen, P.I. J. Biol. Chem. 270, 3869-3875, 1995
A;Title: Sequence, genomic organization, and expression A;Reference number: A55882; MUID:95181349; PMID:7876132
A;Accession: A55882
                                                                                                                                                                                                                                          N;Alternate names: homeotic protein HES-1
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
C;Accession: A55882; S35540; A55802; S355402; A55802; A55802; S355402; A55802; A55802; S355402; A55802; A5580
                                                                                                                                                                                                                                                                                                                                                                              RESULT
A55882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Map position: X
A:Introns: 43/3; 85/1; 147/2; 162/3; 222/1
C:Superfamily: unassigned homeobox proteins
C:Keywords: DNA binding; homeobox; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-362 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T24046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T24046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEDKVRVWFKNKRARCRRHQRE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRENGSPSDGTNSPDDNGKRKQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPENMQPRTRRTKFTLLQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPPK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDELEKVFARTHYPDVFTREELATRVQLTEARVQVWFQNRRAKYRKQER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ly: unassigned homeobox proteins; homeobox homology
DNA binding; homeobox; nucleus; transcription regu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
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35.8%;
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 179.5; DB 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from
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Pred. No. 1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                   PIDN:CAA56344.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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362;

27;

Gaps

1:

PID:g510537

novel homeobox

gene

24 - Sep - 1999

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C;Superfamily: fruit fly homeotic protein goosecoid; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;287-343/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAQMQAHVSGAAAGLSGHGHHPHHPHGHPHHPHLGAHHHGQHHLSHLGHG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AASSAEGHVGQGAPGLMGN----MNPEGGVNHEN-GMNRDG-GMIPEGGGGNQEPRQQPQ 82
                                                                                                                                                                                                                                                                                                                                                                                                                              PPPEEPAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGV 142
#sequence_revision 15-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                         RKRRHRTIFTEEQLEQLEATFDKTHYPDVVLREQLALKVDL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: DNA binding; homeobox; nucleus F; 109-165/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: DNA b
F; 67-123/Domain:
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A;Title: Mutations in the paired domain of the human PAX3 gene cause Klein-Waardenburg A;Reference number: A45452; MUID:93190976; PMID:8447316
A;Accession: A45452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 10-May-1996 #text_change 17-Mar-1999
C;Accession: A45452; A56744; B45452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position:
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A; Residues: 1-28;43-326 <MAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-28, 29-306 < HOT>
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A; Residues: 116-151 <
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Map position: 2q35-2q35
Superfamily: paired box transcription factor Pax-3; homeobox homology;
Keywords: DNA binding; homeobox; nucleus; transcription regulation
;67-123/Domain: homeobox homology <HOX>
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Best Local
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QAGANQLMAFNHL
                                                                         H--QRELMLANEL 171
                                                                                                                                                                                                                                                                                                                                                                     GMIP---EGGGGNQEPRQQPQPPPEEPAQAAMEG-----PQ-----PEN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQRE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNSEKDGNPPLHAPDLPSETSFPCPVDHPRPEERAPKYENYFSASETRSLKRELSWYRGR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNQE-----PRQQPQPPPEEPAQAAMEGPQPENMQP-----R 104
                                                                                                                                                  RKORRSRTTFTAEQLEELERAFERTHYPDIYTREELAQRAKLTEARVQVWFSNRRARWRK
                                                                                                                                                                                                                                                                                                GAVPRMMRPGPGQNYPRS--GFPLEKKAKHSIDGILSERASAPQSDEGSDIDSEPDLPLK
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136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 177; DB 2; Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAX3 gene: DNA sequence
PMID:7782066
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C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regu F;95-151/Domain: homeobox homology
                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S69088; NID:g545359; PIDN:AAB29880.1; R;Nohno, T.; Koyama, E.; Myokai, F.; Taniguchi, S.; Ohuchi, F. Bev. Biol. 158, 254-264, 1993
A;Title: The chicken homeobox gene related to Drosophila pair A;Reference number: I50413; MUID:93321789; PMID:8101172
A;Accession: I50413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kuratani, S.; Martin, J.F.; Wawersik, S.; Lilly, B.; Eichele, Dev. Biol. 161, 357-369, 1994
A;Title: The expression pattern of the chick homeobox gene gMHo: A;Reference number: 151226; MUID:94148118; PMID:7906232
A;Accession: 151226
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C;Superfamily: unassigned homeobox proteins; homeobox homology; paired box
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mech. Dev. 33, 27-37, 1990
A;Title: The murine paired box gene, Pax7, A;Reference number: I49265; MUID:91265334; A;Accession: I49265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          paired box transcription factor pax7 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #tex
                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-154,156-245 < NOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homeodomain protein - chicken N; Alternate names: homeotic 9
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F;182-238/Domain: homeobox homology <HOX>
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                                                                                                                                                                                   C; Genetics:
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A; Residues: 1-245 < KUR>
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                                                                                                                                                                                                      A;Cross-references: GB:D13433; NID:g222850; PIDN:BAA02695.1;
                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
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                     Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGGVNHENG------MNRDGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPE 99
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46; Conserv
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45; Conserv
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33.6%;
                                                                                       Abolowou
                17.8%; Score 176; DB 2; 32.9%; Pred. No. 1.4e-06;
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Pred. No. 1.6e
13; Mismatches
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PMID:1982921
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H.; Saito, T
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Mismatches

Indels

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A;Gene: Psx C;Superfamily: mouse placenta-specific homeobox protein; homeobox homology C;Superfamily: mouse placenta-specific homeobox protein; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; placenta; transcription regulation F;151-207/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                      Phox2 homeodomain protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: I48713
C;Accession: I48713
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R;Han, Y.J.: Park, A.R.; Sung, D.Y.; Chun, Gene 207, 159-166, 1998
A;Title: Psx, a novel murine homeobox gene A;Reference number: JC6540; MUID:98172748; A;Accession: JC6540
                                      A;Gene: Phox2
C;Superfamily: unassigned homeobox proteins;
C;Keywords: DNA binding; homeobox; nucleus; t
F;91-147/Domain: homeobox homology <HOX>.
                                                                                                                        A;Cross-references: EMBL:X75014; NID:g402641; PIDN:CAA52923.1; C;Genetics:
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A; Residues: 1-247 < HAN>
A; Cross-references: GB: AF017453
C; Comment: This protein is involved
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C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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A; Residues: 1-280 < RES>
                                                                                                                                                                                                                            A;Title: The mouse homeodomain protein Phox2 regulates Ncam promoter activity in concert A;Reference number: I48314; MUID:94244481; PMID:7910552 A;Accession: I48713
                                                                                                                                                                                                                                                                                          R;Valarche, I.; Tissier-Seta, J.P.; Hirsch, M.R.; Martinez, S.; Development 119, 881-896, 1993
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  17.8%;
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Pred. No. 1.4e-06;
3; Mismatches 41
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Score 176;
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paired box transcription factor Pax-6 - Ribbonworm C:Specles: Lineus sanguineus (ribbonworm) C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 C:Accession: JC6130
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                                                                                                                                                                                                                                                                    C;Superfamily: unassigned homeobox proteins;
C;Keywords: DNA binding; homeobox; nucleus;
F;47-171/Domain: paired box homology <PBH>
                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X95594; NID:g1296835; PIDN:CAA64847.1; A;Note: the authors translated the codon GCC for residue 338 as C;Comment: This factor is a key regulator of eye morphogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Loosli, F.; Kmita-Cunisse, M.; Gehring, W.J. Proc. Natl. Acad. Sci. U.S.A. 93, 2658-2663, 1996 A;Tille: Isolation of a Pax-6 homolog from the ribbonworm A;Reference number: JC6130; MUID:96181462; PMID:8610097 A;Accession: JC6130
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A;Gene: Pax-6
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A; Residues: 1-370 <LOO>
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IGNM	N Se de	1 57-351-7 57-351-7 57-351-7 TREE TO APPLICATION US/0895735 t NO. 6306586  PALL INFORMATION: Elena PLICANT: MUTTAY, Jeffrey C. PLICANT: METHODS AN THE OF INVENTION: DIAGNOSIS MBER OF SEQUENCES: 33 RRESPONDENCE ADDRESS: ADDRESSEE: FOLEY, HOAG & ELI STREET: One Post Office Squa CITY: BOSTON MPUTER READABLE FORM: MEDIUM TYPE: Flopy disk MEDIUM TYPE: Flopy disk MEDIUM TYPE: FLOPY disk MEDIUM TYPE: FORD: MEDIUM TYPE: PC-DOS/MS- SOFTWARE: PATCHIN Release # RRENT APPLICATION NUMBER: US/08/95 FILING DATE: 24-OCT-1997 CLASSIFICATION: A35 TORNEY/AGENT INFORMATION: NAME: Arnold, Beth E. TELEPHONE: 617-832-1000 REFERENCE/DOCKET NUMBER: UIA LECOMMUNICATION INFORMATION: REGISTRATION NUMBER: UIA LECOMMUNICATION INFORMATION: TELEPAX: 617-832-1000 RMATION FOR SEQ ID NO: 7: QUENCE CHARACTERISTICS: LENGTH: 302 amino acids TYPE: amino acid TOPOLOGY: linear LECOLLE TYPE: protein 57-351-7		D 4 α α α α α α α α α α α α α α α α α α
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          GENERAL INFORMATION:
APPLICANT: Semina
APPLICANT: Murray
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                          142 VTEDKVRVWFKNKRARCRRHQR 163
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                                                                                                                                                                                                                                                             86
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REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 24-OCCCLASSIFICATION: 43
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                                                                                                                                                                                                                           41 SEKASASLPGGSPEDGSLKKKQRRQRTHFTSQQLQELEATFQRNRYPDMSTREEIAVWTN 100
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                                                                                                                                                                                                                                                                                                                        26 QLGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPP 85
                                                                                                                                                                                                                                                                                                                                                                           Local
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One Post Office Square
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          Semina,
Murray,
                                                                                                                                                                                                                                                                                                                                                          19.3%; Score 190.5; DB 4 ilarity 34.5%; Pred. No. 1.5e-11; Conservative 23; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           617-832-7000
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                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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                         Elena
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          Jeffrey C.
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DIAGNOSIS AND TREATMENT (
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                     COUNTRY:
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                                                                                                                                                                        ADDRESSEE:
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Boston

One Post Office

HOAG & ELIOT LLP

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USA

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US-08-957-351-3
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                                                                                  Sequence 3, Application US/08957351 Patent No. 6306586 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 34.5
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
NAME: Arnold, Beth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
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NUMBER OF SEQUENCES:
                TITLE OF INVENTION:
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                                                                                                                                                                                                                                               142 VTEDKVRVWFKNKRARCRRHQR 163
                                                                                                                                                                                                                                                                                                                     86 EEPAQAAMEGPQPEN----MQPRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLG 141
                                                                                                                                                                                                                                                                                                                                                                                         26 QLGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPP 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 35,
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                                                   Murray,
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                                                                    Semina,
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N: 435
              Jeffrey C.
METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF CATARA
                                                                     Elena
                                                                                                                                                                                                                                                                                                                                                                                                                                            19.2%;
34.5%;
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Pred. No. 1.9e-11;
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                  OF CATARACTS
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RESULT 6
US-08-957-351-27
; Sequence 27, Application US/08957351
; Patent No. 6306586
; GENERAL INFORMATION:
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; ORGANISM: mouse
US-09-129-888-2
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/129,888B
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 6
SOFTWARE: WordPerfect 6.1 Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CHUN, Jong Yoon
APPLICANT: HAN, Yun Jeong
TITLE OF INVENTION: Placenta trophoblast-specific gene
FILE REFERENCE: 1942/29
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REFERENCE/DOCKET NUMBER: UII
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
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                                                                                                                                                         150 WEKNKRARCRRHQRELM 166
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                                                                                                                               197
                                                                                                                                                                                             137 SIRNPHVLNRLAQLRYRRTRFTHSQLHDLERLFQETRYPSLRARRDLARWMGVDECDVQN 196
                                                                                                                                                                                                                                                                                          34 EG-HYGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGG-NQEPRQQPQPPPEEPAQA 91
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CLASSIFICATION:
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                                                                                                                               WFRMRRALFQRNRRVLM 213
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                                                                                                                                                                                                                                                                                                                                               Score 176; DB 3;
Pred. No. 3.3e-10;
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US-08-957-351-26
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                                                                                                                                                                                                                                                                                                       Patent No.
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                                                                                                                                                                                                                                                                                          GENERAL
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INFORMATION FOR SEQ ID NO:
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                      APPLICANT: Semina, Elena
APPLICANT: Murray, Jeffrey C.
TITLE OF INVENTION: METHODS A
TITLE OF INVENTION: DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,
                                                                                                                                                                            ADDRESSEE: FOLEY, HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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APPLICANT: Murray, Jeffrey C.
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                      110 QRNRYPDMSMREEIAVWTNLTEPRVRVWFKNRRAKWRKRERNQQL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 DGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVF 122
                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
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                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 35,430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: FOLEY, no.... ADDRESSEE: FOLEY, no... STREET: One Post Office Square
                                                                                              ZIP:
                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/957,351
FILING DATE: 24-OCT-1997
                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                         26, Application US/08957351
o. 6306586
                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                           02109-2170
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APPLICATION DATA:
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37.1%;
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                                                                                                                                                                                                                         METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF CATARA
                                                                                                                                                                            HOAG & ELIOT LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOAG & ELIOT LLP
               Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 173.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 8.2e-10;
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APPLICATION NUMBER: FILING DATE: 24-OCT

24-OCT-1997

US/08/957,351

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RESULT 8
US-08-775-009-37
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Best Local Similarity
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                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                          REFERENCE/DOCKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: No. 5935783el Genes Mapping TITLE OF INVENTION: Veliocardiofacial Syndrome N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 ESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQR 163
TYPE: amd TOPOLOGY:
                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 27-DE CLASSIFICATION: 43
                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 GMNRDGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPENMQPRTRRTKFTLLQVEEL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-024.01
                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5935783ris, LLP
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TWDE: amino acid
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                              ENGTH:
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               amino acid
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(215) 56
                               205 amino acids
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36.2%;
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Pred. No. 1.7e-09;
9; Mismatches 29
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Minimal Critical
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; LOCATION: (117)..(177)
; OTHER INFORMATION: homeobox
US-09-636-735A-2
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                                                                    SOFTWARE: PatentIn version
SEQ ID NO 12
LENGTH: 240
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Berg, Patricia
TITLE OF INVENTION: NO. 64169
FILE REFERENCE: 179.37405X00
                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                    Sequence 12, Application US/09636735A
Patent No. 6416956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 45; Conserv
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Best Local 9
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                                                                                                                                          APPLICANT: Berg, Patricia
TITLE OF INVENTION: NO. 64165
FILE REFERENCE: 179.37405X00
CURRENT APPLICATION NUMBER: U
CURRENT FILING DATE: 2000-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 179.37405X00 CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2000-0
                                                                                                                         NUMBER OF SEQ ID NOS:
                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Homo sapiens
                 FEATURE
NAME/KEY: HELIX 1
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                                                                                                                                                                                                                                                                                                                                                                                                      116 EELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRR 160
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nes 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 SVYQVKISPT----PQLGAASSAEGHV------GQGAPG--LMGNMNPE------GGVN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 PRAAPCGPPEAAAGLGARLAWPLRLGPAVPLSLGAPAGGSGALPGAVGPGSQRRTRRHRT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 PROOPOPPEEPA----RT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HENGMURDGGMIPEGGGGUQEPRQQPQPPPEEPAQAAMEGPQPEUMQPRTRRTKFTLLQV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                          HPQELEAD-----SEKPRLSPEPSERRPQAPAKKLRKP-----
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27.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 240;
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Query Match
Best Local Similarity 52...
Thes 31; Conservative
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US-08-775-009-38
                                                                                             US-08-775-009-38
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                                                                                                                                                                                                                          TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (144)...
NAME/KEY: HELIX 3
LOCATION: (158)...
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION UNMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-(
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                            MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. 5935783el Genes Mapping in the TITLE OF INVENTION: Vellocardiofacial Syndrome Minimal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: One La CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 27-DEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 AAYPLGLSPTTAASPNL-SYSRPYGHLLSYPYTEPANPGDSYLSCQQPAALSQPLCGPAE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 SVYQVKISPT----PQLGAASSAEGHV------GQGAPG--LMGNMNPE------GGVN 55
                                                                                                                                           TOPOLOGY:
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Local Similarity 27.3%;
les 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPQELEAD------SEKPRLSPEPSERRPQAPAKKLRKP-----RTIYSSLQL 129
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Pred. No. 1.1e-08;
N4 smatches 52;
                         Score 160; DB 2;
Pred. No. 2.2e-09;
2; Mismatches 16;
                                                       Length 60
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US-08-958-642-4
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LENGTH: 99
TYPE: PRT
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     Matches
                     Query Match
Best Local
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APPLICANT:
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TITLE OF INVENTION: Methods and Compositions for Enhancing
TITLE OF INVENTION: Osseous Growth, Repair, and Regeneration
                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: WFU98-18
CURRENT APPLICATION NUMBER: US/09/031,962D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NO
TITLE OF INVENTION: DII
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                             FILING DATE:
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   Local Similarity les 41; Conserv
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                                                                                                                                      LENGTH:
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es 31; Conserv
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                                                                                                                      amino acid
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ber 31, 1996
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     18;
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Score 158; DB 2; L
Pred. No. 4.7e-08;
Pred. No. 4.7e-08;
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                                                                                                                                                                                                                                                                                              Version #1.30 (EPO)
                                   Length 436;
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US-08-778-423A-4
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US-08-778-394-2
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Best Local Similarity 30.8
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SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: NOVEL METHOD FOR TESTING THE TITLE OF INVENTION: DIFFERENTIATION STATUS IN PANCREAT! NUMBER OF SEQUENCES: 16

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,423A
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MEDIUM TYPE: Floppy disk
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281 REEK---LRNQRR 290
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FILING DATE:
CLASSIFICATION: 514
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Search completed: April 28, 2003, 04:05:27 Job time: 33 secs
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Best Local Similarity
Watches 41; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: December 31, 1996
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                  281
                                                                                              160 RHORELMLANELR 172
                                                                                                                                                               100 MMQPRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCR 159
                                                                                                                                                                                                184 GQPTQDGCQQQEGGGENTNSISSNG-----
                                                                                                                                223 KLQ--RNRTSFTQEQIEALEKEFERTHYPDVFARERLAAKIDLPEARIQVWFSNRRAKWR 280
                                                                                                                                                                                                                               40 GAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPE 99
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)GY: linear
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30.8%;
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Pred. No. 4.7e-08;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Blaschke R.J., Monaghan A.P., Schiller S., Schechinger B., Rao E., Padilla-Nash H., Ried T., Rappold G.A.; "SHOY. related homeobox gene, is implicated in craniofacial brain, heart, and limb development.";

craniofacial

Sci. U.S.A. 95:2406-2411(1998).

Strausberg R.; ISSUE=Muscle; SEQUENCE FROM N.A.

(MAY-2001) to the EMBL/GenBank/DDBJ databases

SEQUENCE FROM N.A. (ISOFORMS 1 AN TISSUE-Fibroblast; MEDLINE-98151525; PubMed-9482898;

(ISOFORMS 1 AND

HUMAN 2; 0609 T-2001 T-2001 T-2002 Status (Homec OR SHC Sapiens Yota; N	RESULF 1 SHX2_HUMAN	44 173 17.5 45 173 17.5	173.5 17.	173.5 17.	5 17.	176 17.		176 17.	176 17		176.5 17	
STANDARD; 03; 060465; 060467; (Rel. 40, Created) (Rel. 40, Last seque) (Rel. 41, Last anno e homeobox protein box protein 0912X).		247 1 292 1			284 245							
STANDARD; PRT; 331 AA. 103; O60465; O60467; (Rel. 40, Created) (Rel. 41, Last sequence update) (Rel. 41, Last annotation update) re homeobox protein 2 (Paired-related homeobox protein bbox protein Ogl2X). 9T OR OGl2X. 13 (Human).	ALIGNMENTS	PMX2_MOUSE PIX3_XENLA	PIX2_CHICK	PIX1_MOUSE	GSC CHICK	PAX3_MOUSE	PAX3_HUMAN	PMXA_RAT	PMXA_MOUSE	PMX1_CHICK	PIX1_DROME	
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"A new human homeobox gene OG12X is a l MEDLINE=98133920; PubMed=9466998; FISSUE=Craniofacial; SEQUENCE OF 116-331 FROM N.A. (ISOFORM nomeobox gene family and n. Mol. Genet. 7:415-422(1998).

FUNCTION: May be a growth regulator and have a role in specifying neural systems involved in processing somatosensory information, as well as in face and body structure formation.

SUBCELLULAR LOCATION: Nuclear.

SUBCELLULAR PRODUCTS: 2 isoforms; 1/SHOX2A/SHOTA (shown here) and 2/SHOX2B/SHOTB/OG12XB; are produced by alternative splicing.

2/SHOX2B/SHOTB/OG12XB; are produced by alternative splicing.

TISSUE SPECIFICITY: Expressed in heart, skeletal muscle, liver, lung, bone marrow fibroblast, pancreas and placenta.

DEVELOPMENTAL STAGE: Expressed during cranofacial development as Well as in heart.

SIMILARITY: BELONGS TO THE PAIRED HOMEO
"BICOID" SUBFAMILY.

SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.

SIMILARITY: CONTAINS 1 OAR DOMAIN. TO THE PAIRED HOMEOBOX FAMILY. ne OG12X is a member is expressed during 2). There are no restrictions on it is as its content is in no ... of the e most conserved development in in specifying
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Matches 56
                                                                                                                                                                 _CHICK
                                                                                            09PVX0;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Retinal homeobox protein Rx2 (CRax2).
                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
Erchosauria; Aves; Neogn
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PROSITE; PS50803; OAR; 1.
Homeobox; DNA-binding; Developmental
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EMBL; AJ002368; CAA05342.1;
EMBL; BC008829; AA0108829.1;
EMBL; AF022654; AAC39662.1;
EMBL; AF023203; AAC39663.1;
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PRINTS; PR00031; HTHREPRESSR.
PRODOM; PD0000010; Homeobox; 1
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InterPro; IPR003654; Homeo_OAR.
InterPro; IPR001356; Homeobox.
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TRANSFAC; T04224; -
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an email to license@isb-sib.ch)
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PubMed=10415362
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POLY-GLY.

POLY-GLY.

MISSING (IN ISOFORM SHOX2B).

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E -> D (IN REF. 1; CAA05341).

P -> S (IN REF. 2).

D -> N (IN REF. 2 AND 3).

H -> L (IN REF. 3; AAC39663).

MW; 55431B073B3B2250 CRC64;
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PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50803; OAR; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P06601; 1FJL.
InterPro; IPR003554; Homeo_OAR.
InterPro; IPR003556; Homeobox.
InterPro; IPR001356; Homeobox.
1.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB020318; BAA84749.1; -. HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
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SUBCELLULAR LOCATION: Nuclear (By similarity).

DEVELOPMENTAL STAGE: Expressed at stage 4 in the ectoderm, stage 6 in the anterior most neural plate, at stage 7 and anterior neural fold and at stage 9-10 in the evaginating vesicles. At stage 14, highly expressed in developing retination in find the stage 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN. SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in infundibulum region.
SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY "BICOID" SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCLPKGPAEPPPAEHQGRFQEPYCPGSASPELPAGDGGDGKPSDEEQPKKKHRRNRTTFT
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                                                                                                     P70369;
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294
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l (Rel. 40,
l (Rel. 41,
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                                                                                                                               STANDARD;
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181
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29.3%;
Last sequence update)
Last annotation update)
x protein 2 (Homeobox pr
                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 202.5;
Pred. No. 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMEOBOX.
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                                                                                                                               331
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les 61;
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subsequent
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Short stature

(Homeobox protein

0g12X)

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Rovescalli A.C., Asoh S., Nirenberg M.W.;
"Cloning and characterization of four murine homeobox genes.";
Proc. Natl. Acad. Sci. U.S.A. 93;10691-10696(1996).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc.
                  TRANSFAC; T03310; --
TRANSFAC; T04233; --
MGD; MGI:1201673; Shox2.
MGD; IPR003654; Homeo_OAR
InterPro; IPR001356; Homeobox.
                                                                                  EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      van Schaick H.S.A., Smidt M.P., van der Kleij A.A.M., Asoh S.,
                                                                                                                                                            modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                    use
                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BALB/c; TISSUE-Liver, and MEDLINE-97008065; PubMed-8855241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98058757; PubMed=9371788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Paired family homeodomain SHOX2 OR OG12X OR PRX3.
                                                                                                                                                                                                                                                                                                                                                    +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Semina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL EXPRESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissues
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                                                                          HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homeobox gene family and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Homeobox gene Prx3 expression in rodent
                                                                                                                                                   send an email to license@isb-sib.ch).
                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBI outstation - Buropean Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                       L; U66918; AAC52833.1; -.
L; U67055; AAC52834.1; -.
L; U65071; -; ANOTATED_CDS.
L; U65072; AAC52831.1; ALT_INIT.
L; U65072; AAC52832.1; ALT_INIT.
P; P06601; 1FJL.
                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX "BICOID" SUBFAMILY.
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       PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E.V., Reiter R.S., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genet. 7:415-422(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reiter R.S., Murray J.C.;
homeobox gene OG12X is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Mouse)
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                               Homeo_OAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                м.Р.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kozak C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rovescalli A.C., Luijten M
Kozak C.A., Nirenberg M.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Embryo;
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RESULT 4

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15-JUL-1998
15-JUL-1998
15-JUN-2002
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VARSPLIC
SEQUENCE
                                                          entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gan L.,
Klein W.
  EMBL;
HSSP;
                                                                                                                                                                                                                                                                                FUNCTIONS IN THE DEVELOPING EMBRYOS.
-!- SUBUNIT: BINDS DNA AS A MONOMER.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DEVELOPMENTAL STAGE: FOUND INITIALLY IN .
EMBRYO, BUT GRADUALLY BECOMES RESTRICTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strongylocentrotus purpuratus (Purple sea urchin)
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; I
Echinoidea; Euechinoidea; Echinocea; Echinoida; S'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50803; OAR; 1.
Homeobox; DNA-binding; Developmental protein;
                                                            use by non-profit institutions as long modified and this statement is not removed: entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                        This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinf the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTX_STRPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=95180495; PubMed=7875376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strongylocentrotus.
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                                                                                                                                                                                                                                                                                                                                                                                . Biol. 167:517-528(1995).
FUNCTION: MAY PLAY A ROLE IN ACTIVATION OF TO THE TAATCC MOTIF WITH HIGH SPECIFICITY.
                                                                                                                                                                                                                                          ENDODERM CELLS.
SIMILARITY: BELONGS
                                                                                                                                                                                                                       "BICOID" SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RQQPQPP-----PE----EPAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVF
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  S76899;
P06601;
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331 AA;
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  AAB33568.1;
1FJL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 36, Created)
. 36, Last sequence update)
. 41, Last annotation updat
OTX (SPOTX).
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326
82
246
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Pred. No. 5.
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OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                   ght. It is produced through Bioinformatics and the EM titute. There are no restr
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                                                                                                                                                                                                                                            HOMEOBOX
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D TO
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ORAL E
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HAVE ADDITIONAL
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                                                                                                                                                                 a collaboration -
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PIX3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 52; Conser
DEVELOPMENT.

DEVELOPMENT.

-!- SUBCELLULAR LOCATION: Nuclear (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear (By similarity).

-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN DEVELOPING EYE LENS.

-!- DISEASE: MUTAFIONS IN PITX3 APPEAR TO BE THE CAUSE OF THE ANTERIOR SEGMENT MESENCHYMAL DYSGENESIS (ASMD) AND AUTOSOMAL-DOMINANT CONGENITAL CATARACTS (ADDC). ASMD INCLUDES ALL MALFORMATIONS INVOLVING THE FIRST (CORNEAL ENDOTHBLIUM AND TRABEGULAR MESHWORK), SECOND (CORNEAL STROMA) AND THIRD (IRIS STROMA) MESENCHYMAL WAVES OF NEURAL CREST. THE ASMD PHENOTYPE IS CHARACTERIZED BY CORNEAL OPACITIES WITH OR WITHOUT IRIS ADHESIONS IN 100%, CATARACTS OF VARYING SEVERITY IN 100% AND OPTIC-NERVE ABNORMALITIES IN 20% OF AFFECTED INDIVIDUALS. ADCC IS CHARACTERIZED BY DOMINANT TRANSMISSION OF A PHENOTYPE CONSISTING OF BILATERAL CONGENITAL CATARACTS IN A MOTHER AND SON WITHOUT CLINICAL ANTERIOR-SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, C
15-JUL-1999 (Rel. 38, I
15-JUN-2002 (Rel. 41, I
Pituitary homeobox 3 (Herrica)
PITX3 OR PTX3.
                                                                                                                                                                                                                                                                                                            Nat.
[2]
                                                                                                                                                                                                                                Strausberg R.;
                                                                                                                                                                                                                                                                                                                        dominant cataracts and ASMD.";
Nat. Genet. 19:167-170(1998).
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANT ADCC ASN-13.
TISSUE-Craniofacial;
MEDLINE-99282095; PubMed-9620774;
Semina E.V., Ferrell R.E., Mintz-Hittner H.A.,
Semina E.V., Ferrell R.E., Funkhauser C., Daac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEOBOX, 2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein.
DNA_BIND 131 190 HOMEOBOX.
SEQUENCE 371 AA; 41215 MW; B6BD493D684A33F7 CRC64;
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InterPro;
                                                                                                                                                                                                                                                                             TISSUE=Muscle;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                      "A novel
                                                                                                                                                                                                                                                                                                                                                                     Murray J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          075364;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139
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Chordata;
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29.9%;
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Last annotation
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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n PITX3).
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ALX4_MOUSE
ID ALX4_M
AC 035137
DT 16-OCT
DT 15-UN
DE HOMEOD
GN ALX4.
OS Mus mu
OC Eukary
OC Mammal
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Best Local
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                                                                                                                                                                                                                                                                                                         ALX4_MOUSE
035137;
                                                                                                                                                                                                                                    16-OCT-2001
16-OCT-2001
15-JUN-2002
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox
SMART; SM00389; HOX; 1.
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    STRAIN=C57BL/6; T
MEDLINE=98086222;
                                                                                                                     Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                            SEQUENCE FROM N.A.
                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                Homeobox protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEPAQAAMEGPQPEN----MQPRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFGLLSEAEAR----SPALSLS---DAGTPHP-----QLPEHGCKGQEHSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTEARVRVWFKNRRAKWRKRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEKASASLPGGSPEDGSLKKKQRRQRTHFTSQQLQELEATFQRNRYPDMSTREEIAVWTN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF041339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC011642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation.
                                                                                                                   Eutheria;
                                                                                                                                                                                                              (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
otein aristaless-like 4 (ALX-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
TISSUE=Embryo;
2; PubMed=9426253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC24502.1;
AAH11642.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
275
250
272
13
                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homeo_OAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 190.5; DB 1
Pred. No. 3.5e-07;
3; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OAR.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEAR LOCALIZATION S -> N (IN ADCC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR_003767.
1E5259206ABC2E87 CRC64;
                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                    399
                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302;
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Best Local S
Matches 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene
                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                             PROSITE; PS50803; OAR; 1.

Homeobox; DNA-binding; Developmental protein; Nuclear Transcription regulation; Activator; Disease mutation
                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000010;
SMART; SM00389; HO
PROSITE; PS00027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF001465; AAC39943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polydactyly.";
Development 125:2711-2721(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qu S., Tucker S.C., E
Wisdom R., Vogt T.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98301426; PubMed=9636085;
Qu S., Tucker S.C., Ehrlich J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homeodomain protein
                                                                                                                                                                                                                                                                                                 DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003654; Homeo_OAR.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WGD; MGI:108359; Alx4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFAC; T02967; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mutations in mouse Aristaless-like4 cause Strong's luxoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT LST GLN-206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Alx-4: cDNA cloning and homeodomain protein ":
                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00046;
   103
                                  140
                                                                80
                                                                                                95
                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REDUCTIONS AND DUPLICATIONS OF THE RADIUS, ABSENCE OF THE TIBIA, CRANICIPACIAL DEFECTS, REDUCTION OF THE PUBIS, AND DORSAL ALOPECIA. SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY. SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: EXPRESSED IN OSTEOBLASTS. NOT EXPRESSED IN BRAIN, HEART, INTESTINE, KIDNEY, LIVER, MUSCLE, SPLEEN AND TESTIS. DEVELOPMENTAL STAGE: EXPRESSED FROM E8.25 AND CONFINED TO MESENCHYMAL CELLS THROUGHOUT THE EMBRYO DEVELOPMENT. EXPRESSION IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEEN AT SEVERAL SITES INCLUDING CRANIOFACIAL REGION, FIRST BRANCHIAL ARCH AND ANTERIOR ASPECT OF THE LIMB BUD.

DISEASE: DEFECTS IN ALX4 ARE THE CAUSE OF STRONG'S LUXOID (LST) PHENOTYPE. AT HETEROZYGOSITY LST IS CHARACTERIZED BY PREAXIAL ABNORMALITIES OF THE HINDFEET AND, VERY RARELY, OF THE FOREFEET HOMOZYGOTES SHOW PREAXIAL POLYDACTYLY OF ALL FOUR LIMBS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: BINDS DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENT
                                VPCYAKESNLGEPELPPDSEPVGMDNSYLSVKETGAKGPQDRASAEIPSPLEKTDSESNK 199
                                                                                                                             PTPQ---LGAASSAEGHVGQGAPGLMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQ 79
-- PRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRR
                                                                                               PTPQPPPAPPAHLYLQRGA----CKTPPDGSLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P06601;
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                           PS00027; HOMEOBOX_1; 1.
PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wisdom R.;
                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                           homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                              XOH,
                                                                -QPPPEEPA-----QAAMEGPQ-----PENMQ-----
                                                                                                                                                                                                                                                                261
392
206
                                                                                                                                                                                                                                42762 MW;
                                                                                                                                                                               19.2%;
30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FACTOR INVOLVED IN SKULL AND LIMB
                                                                                                                                                                             Score 189.5;
Pred. No. 5.
                                                                                                                                                                                                                                            R -> Q (IN LST; ABOLISHES DNA BINDING TRANSCRIPTIONAL ACTIVATION).
                                                                                                                                                                                                                                                                                OAR.
                                                                                                                                                                                                                                                                                               HOMEOBOX.
                                                                                                                                                                                                                              2EDE19DDACA21D25 CRC64;
                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levorse J.M., Flaherty L.A.,
                                                                                                                                                                             .5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of a
                                                                                                                                                                                            DB 1;
                                                                                                                                                               49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    novel paired-type
                                                                                                                                                                                            Length
                                                                                                                                                               Indels
                                                                                             -LQEGSGGHNAALQ 139
                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                              399;
                                                                                                                                                               57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       outstation
                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murray J.C.;
Murray J.C.;
"A novel homeobox gene PITX3 is
"A novel homeobox gene PITX3 is
dominant cataracts and ASMD.";
Nat. Genet. 19:167-170(1998).
Nat. Genet. 19:167-170(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIX3_MOUSE 035160;
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                 phenotype, a recessive homozygous
eyes and closed eyelids.
-i- SIMILARITY: BELONGS TO THE PAIRED
"BICOID" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98282096; PubMed=9620774;
Semina E.V., Ferrell R.E., Mintz-Hittner H.A., Bitoun
Alward W.L.M., Reiter R.S., Funkhauser C., Daack-Hirso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1902 (Rel. 41, Last annotation update)
Pituitary homeobox 3 (Homeobox protein PITX3)
                                                                                        EMBL; AF005772;
HSSP; P06601; 1
                                                                                                                                                    modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Embryo, and Embryonic carcinoma; MEDLINE=97472463; PubMed=9328475;
                                          InterPro;
                                                                                                                                       or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Genet. 19:16/-1/0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on mouse chromosome 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation of a new homeobox gene belonging to the Pitx/Rieg family: expression during lens development and mapping to the aphakia region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Semina E.V., Reiter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                           TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 RER 262
                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN. SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                muscles.
DISEASE: Mutations in PITX3 appear to be the cause of the aphakia phenotype, a recessive homozygous disease characterized by small
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: Highly expressed in developing eye lens. DEVELOPMENTAL STAGE: First expressed in the eye in day E10 post-coitum embryos. Throughout eye development, expressed in tens placode and forming lens pit. From day E12, also detected the midbrain region, tongue, incisor primordia, condensing
                                                                                                                                                                                                                                                                                                                                                                                           mesenchyme around the sternum and vertebrae and
                                                            SFAC; T02666; -.
MGI:1100498; Pitx3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HQR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lens development
                           IPR003654; Homeo_OAR IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet. 6:2109-2116(1997).
                                                                                                                                      equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                         1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                          AAB87380.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murray J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                 HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    normal eye
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                                                                                                                                                                      Usage
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L outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Hypothalamus;
MEDLINE-98058810; PubMed-9371841;
Smidt M.P., van Shaick H.S.A., Lanctot C., Trem
Smidt M.P., van Shaick H.S.A., Lanctot C., Trem
van der Kleij A.M., Wolterink G., Drouin J.,
"A homeodomain gene Ptx3 has highly restricted
mesencephalic dopaminergic neurons.";
Proc. Natl. Acad. Sci. U.S.A. 94:13305-13310(19)
                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, 30-MAY-2000 (Rel. 39, 15-JUN-2002 (Rel. 41,
 TRANSFAC;
            EMBL; AJ011005; CAA09455.2; HSSP; P06601; 1FJL.
                                              or send
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                                                                                                                                                                                                 <del>: :</del>
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PITX3 OR PTX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P81062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIX3_RAT
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                 REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                  SUBCELLUAR LOCATION: NUClear.
TISSUE SPECIFICITY: Restricted to mesencephalic do system (MESDA).
SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY.
"BICOID" SUBFAMILY.
SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                     s SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is iffied and this statement is not removed. Usage by and fo ities requires a license agreement (See http://www.isb-sib.
                                                                                                                                        SIMILARITY: CONTAINS 1 HOMEOBOX DO SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPEN----MQPRTRRTKFTLLQVEELESVF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPEHGCKGQEHSD-----SEKASASLPGGSPEDGSLKKKQRRQRTHFTSQQLQELEATF 81
                                            s requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD000010;
                                                                                                                                                                                                                                                                               TO 66; 108; 122 AND 132-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homeobox 3 (Homeobox protein PTX3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
          1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.1%;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 188; DB 1;
Pred. No. 5.3e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-ALA.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                      94:13305-13310(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                         There are no restrictions
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                                                                                                                                                                                                                                                                                                                                      Tremblay
                                                       http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Indels
                                                                                                                                                                                                                                                                                                                            brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
                                                                                                                                                                                                                                                                                                                                      mblay J.T., Cox
Burbach J.P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                dopaminergic
                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                            expression
                                                                                                                                                                                                                                                                                                                                                                                                                    Murinae;
                                                                                                                                                                                                                                                                                                                                                  Cox J.J.,
                                                                                                       a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                     for
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                                                                     commercia
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RESULT 9
CRX_BOVIN
QY
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                              "Interaction of phosducin and PhLOP1 with CRX: potential transcriptional regulation function."; submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS AND TRANSACTIVATES THE SEQUENCE 5'-TAATC[CA]-3'
WHICH IS FOUND UPSTREAM OF SEVERAL PHOTORECEPTOR-SPECIFIC GENES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50803; OAR; 1.
PROBITE; PS50803; OAR; 1.
HOMEOBOX; DNA-binding; Developmental
DNA_BIND 62 121 HOMEOBOY
                                                                                                 or send an email to license@isb-sib.ch)
                                                                                                             modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                   the
                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                         TISSUE-Retina;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cone-rod homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9XSK0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRX_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00389; HOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00024; HOMEOBOX. ProDom; PD000010; Homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003654; Homeo_OAR
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                               Zhu X., Craft C.M.;
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                            Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
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                                                                                                                                                                                                   SUBCELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: RETINA.
SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY.
                                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                                                                                         INCLUDING THE OPSIN GENES. ESSENTIAL MAMMALIAN PHOTORECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPEHGCKGQEHSD-----SEKASASLPGGSPEDGSLKKKQRRQRTHFTSQQLQELEATF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRNRYPDMSTREEIAVWTNLTEARVRVWFKNRRAKWRKRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
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                                                                                                                                      non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                          Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262
240
268
302
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                                                                                                                                                                                                                                                                                                                                                                                          Bos.
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41,
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250
272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation
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POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 188;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
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                                                                                                                                                  There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3e-07
                                                                                                             http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                      THE
                                                                                                                          Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163
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                                                                                                                                                                                                                                                      MAINTENANCE
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                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
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                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                       Bovoidea;
                                                                                                                                                                a collaboration -
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Pfam; PF00046; homeobox; ProDom; PD000010; Homeobo TRANSFAC; T03489; ...
InterPro; IPR001356; Homeobox.

Homeobox;

SM00389; HOX;

EMBL; AF154123; HSSP; P06601; 1E

AAD34645.1;

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RESULT 10
GSC_HUMAN
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                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFAC; T04037; -. Genew; HGNC:4612; GSC. MIM; 138890; -. Interpr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSC_HUMAN
P56915;
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                                                                                                                                                                                                                                                                        PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Developmental protein; Nuclear protein; DNA-binding; Homeobox.
DNA_BIND 155 214 HOMEOBOX.
SEQUENCE 252 AA; 27853 MW; 6C0EEC48C084D323 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning of the human homeobox gene goosecoid (GSC) mapping of the gene to human chromosome 14q32.1."; Genomics 21:388-393(194).

-I- FUNCTION: REGULATES CHORDIN (CHRD). MAY PLAY A ROLE IN SPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Geissert D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Leukocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, 30-MAY-2000 (Rel. 39, 15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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DNA_BIND 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; Activator; Homeobox; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94375063;
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    154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 YAREEVALKINLPESRVQVWFKNRRAKCRQQRQQ 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "BICOID" SUBFAMILY.
); P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROGRAMING WITHIN DISCRETE EMBRYONI COMPARTEMENTS DURING ORGANOGENESIS. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS
RKRRHRTIFTDEQLEALENLFQETKYPDVGTREQLARKVHLREEKVEVWFKNRRAKWRRQ
                                          --RTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRH 161
                                                                                                                                    GMIPEGGGGNQEPRQQPQPPEEPAQAAMEGPQPENMQP------
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                                                                                         GAVPPLGA--QQCSCVPTPPGYEGPGSVLVSPVPHQMLPYMNVGTLSRTELQLLNQLHCR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPPEEPAQA-AMEGPOPENMOP------RTRRTKFTLLQVEELESVFRHTQYPDV 130
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                                                                                                                                                                                                          Similarity
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PS50071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94375063; PubMed=7916327;
De Robertis E.M., Kojis T.,
D., Sparkes R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 F
32253 MW;
                                                                                                                                                                                                        18.8%;
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41.5%;
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Last annotation update)
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                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 187; DB 1; Lc. Pred. No. 6.2e-07;
                                                                                                                                                                                                                           Score 185.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMEOBOX.
512ED6A6DAFBAC19
                                                                                                                                                                                                          Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAIRED HOMEOBOX FAMILY
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                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                          No.
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                                                                                                                                                                                                      6.7e-07
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                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                           Length
                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                252;
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RESULT 11
GSC_MOUSE
                                                                          STREET REPRESENTATION OF THE PROPERTY OF THE P
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                      Query Match
Best Local Similarity
                                                                        DNA_BIND SEQUENCE
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Q02591;
                                                                                                                                                                                   Prodom; PDUUUULU; numec
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M85271; AAA37826.1; -. EMBL; Y13149; CAA73611.1; -. EMBL; Y13150; CAA73612.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSC.
                                                                                                                                                                                                                 Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                    PIR; A42768; A42768.
HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blum M., Gaunt S.J., Cho K.W. Bittner D.A., de Robertis E. "Gastrulation in the mouse: Cell 69:1097-1106(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel.
01-FEB-1994 (Rel.
15-JUN-2002 (Rel.
                                                                                              Developmental protein; Nuclear protein; DNA-binding; Homeobox DNA_BIND 160 219 HOMEOBOX.
                                                                                                                                      PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                         MGD; MGI:95841; Gsc
                                                                                                                                                                                                                                                                                                                  TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                goosecoid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98079105; Pub
Danilov V., Blum M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92315328; PubMed=1352187; Blum M., Gaunt S.J., Cho K.W.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Negative autoregulation of the organizer-specific joosecoid.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                     nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTO XENOPUS EMBRYOS.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: IN EARLY G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDUCTION: BY ACTIVIN. SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 273:627-635(1998). FUNCTION: GOOSECOID-EXPRESSING REGIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND BODY WALL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: IN EARLY GOODSAL LIP. IN LATER STAGES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE EGG CYLINDER HAVE ORGANIZER-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "BICOID" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĸ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                     IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                  T02047; -.
                                                                        256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 28, Created)
. 28, Last sequence update)
. 41, Last annotation update)
goosecoid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9417125;
M., Schweickert A.,
                                                                        27979 MW;
  18.8%;
36.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO THE PAIRED HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the role of the
  Pred. No.
                        Score 185.5;
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                                                                        3639FB059AC3DB9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GASTRULATION, OF DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steinbeisser H., Blumberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256
    6.8e-07;
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                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF THE GASTRULATING ACTIVITY WHEN TRANSPLANTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homeobox gene goosecoid. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
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                           256;
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Matches

Conservative

16;

Mismatches

37;

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P54821; 060807;
01-0CT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Paired mesoderm homeobox protein 1 (PRX-1) (Paired related homeobox
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS50803; OAR; 1.
Homeobox; DNA-binding; Developmental
                                                                                                                                                                                                                                                                                                                                      the
                                                                    ProDom; PD000010; Homeo SMART; SM00389; HOX; 1
                                                                                  Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
                                                                                                                 InterPro; IPR003654; Homeo_OAR.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                      Genew;
                                                                                                                                                                                      EMBL; 297200; CAB10073.1; -. EMBL; 297200; CAB10074.1; -. EMBL; 895929; AAA60085.1; -. HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding activity of serum r
Science 257:1089-1095(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grueneberg D.A., Natesan S., Alexandre C., Gilman M.Z., "Human and Drosophila homeodomain proteins that enhance binding activity of serum response factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92376525; PubMed=1509260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                      entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pearce A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein 1) (Homeobox protein PHOX1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219
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                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: ACTS AS A TRÂNSCRIPTIONAL REGULATOR OF MUSCLE CREATINE KINASE (MCK) AND SO HAS A ROLE IN THE ESTABLISHMENT OF DIVERSE MESODERWAL MUSCLE TYPES. THE PROTEIN BINDS TO AN A/T-RICH ELEMENT IN THE MUSCLE CREATINE ENHANCER (BY SIMILARITY).

SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; PMX1-A AND PMX1-B (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY.
SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                        167420;
                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Κ̈́R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAVPPLGA--QQCSCVPTPPGYEGPGSVLVSPVPHQMLPYMNVGTLSRTELQLLNQLHCR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GMIPEGGGGNQEPRQQPQPPPEEPAQAAMEGPQPENMQP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKRRHRTIFTDEQLEALENLFQETKYPDVGTREQLARKVHLREEKVEVWFKNRRAKWRRQ 218
                                                                                                                                                                     HGNC:9142; PMX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A. (ISOFORM PMX1-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                    1FJL.
                                                                                                                                                                                                                                                                                 license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae
   protein;
                                                                                                                                                                                                                                                                                                                                 There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae;
   Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enhance the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
   protein;
                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                  EMBL outstation
                                                                                                                                                                                                                                                                                                                                                       a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-
                                                                                                                                                                                                                                                                                                     for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative
DNA_BIND
   "rHox: a
J. Cell.
                                                                                                                                                                                                                                                                               "MHOX: a mesodermally restricted homeodomain protein that binds an essential site in the muscle creatine kinase enhancer."; Development 115:1087-1101(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PMX1_MOUSE STANDARD; PRT; 245 AA.
P43271; Q02810;
Q1-FEB-1995 (Rel. 31, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Paired mesoderm homeobox protein 1 (PRX-1) (Paired related homeobox protein 1) (Homeobox protein MhoX) (Homeobox protein K-2) (Rhox).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; MCBI_TaxID=10090, 10116;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse), and Rattus norvegicus (Rat).
                           Morrison N.A.
                                     Hu Y., Flanagan J.,
                                                   MEDLINE=96340959;
                                                                SPECIES=Rat;
                                                                                                             cloning
                                                                                                                                   MEDLINE=93027261; PubMed=1383943; Kern M.J., Witte D.P., Valerius M.T.,
                                                                                                                                                                      SEQUENCE FROM N.A. (PMX1-A ISOFORM)
                                                                                                                                                                                             "Genomic organization and chromosome homeobox gene Pmx."; Genomics 19:334-340(1994).
                                                                                                                                                                                                                                 Kern M.J., Argao E.A., Birkenmeier E.H.,
                                                                                                                                                                                                                                                                                                                                                       SPECIES-Mouse;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (PMX1-A ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRRX1 OR PMX1 OR PMX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                          SEQUENCE FROM N.A.
                                                                                                   Nucleic
                                                                                                                        "A novel murine homeobox gene isolated
                                                                                                                                                                                                                                             MEDLINE=94245205; PubMed=7910581;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (PMX1-A ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 SSAEGHVGQGAPGLMGNMNPEG-------GVNHENGMNRDGGMIP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSSYGHVLERQPALGGRLDSPGNLDTLQAKKNFSVSHLLDLEEAGDMVAAQADENVGEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSLLESPGLTSGSDTPQQD------NDQLNSEEKKKRKQRRNRTTFNSSQLQALERV
               Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L Similarity
49; Conser
                                                                                      strategy.";
arids Res. 20:5189-5195(1992).
  Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245
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94 15:
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197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                            STRAIN=CD-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GGNQEPRQQPQPPPEEPAQAAMEGPQPENMQPRTRRTKFTLLQVEELESV
gene expressed in osteoblastic cells.";
59:486-497(1995).
                                                  PubMed=8749718;
                                                                        (PMX1-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153
235
197
245
                                      Brennan D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27296 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.7%;
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3 HOMEOBOX.
                                                                           ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 184.5; DB 1
Pred. No. 7.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (POTENTIAL).
SAMATYSATCANNSPAQGINMANSIANLRLKAKEYSLQRNQ
VPTVN -> RSSSLPRCCLHEGLHNGF (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PMX1-A)
                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7CA4B7FD9492FC19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                      Zhou
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                                                                                                                        bу
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                                      K.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                       Potter S.S.; specific PCR
                                      Eisman
                                                                                                                                                                                                                                Potter S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160
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                                     J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
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RESULT 14
AL_DROME
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X33,1; A
EMBL; S82911; A
USSP; P06601;
T020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T02060; -.
TRANSFAC; T02061; -.
TRANSFAC; T02966; -.
MGD; MGI: 97712; Prix1.
        AL_DROME Q06453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS:PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00389;
PROSITE; PS0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:97712; Prrxl.
InterPro; IPR003654; Homeo_OAR.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00046;
                                                                                                                                                                           113
                                                                                                                                                                                                                               122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            omeobox;
                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                             31 SSAEGHVGQGAPGLMGNMNPEG------GVNHENGMNRDGGMIP------EGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUSCLE, HEART AND UTERUS.
DEVELOPMENTAL STAGE: EXPRESSED DURING CARDIOGENESIS.
SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY.
SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; PMX1-A AND PMX1-B (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN MESODERMALLY DERIVED CELL TYPES. DURING EMBRYOGENESIS, HIGHEST LEVELS OF EXPRESSION ARE FOUND IN THE MESENCHYME AND PRECARTILAGE ELEMENTS OF THE FACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: ACTS AS A TRANSCRIPTIONAL REGULATOR OF MUSCLE CREATINE KINASE (MCK) AND SO HAS A ROLE IN THE ESTABLISHMENT OF DIVERSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND HIND LIMBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MESODERMAL MUSCLE TYPES. THE PRO IN THE MUSCLE CREATINE ENHANCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KINASE (MCK) AND SO HAS A ROLE IN THE
                                                                                                                                                                      FERTHYPDAFVREDLARRVNLTEARVQVWFQNRRAKFRRNER-AMLANK 160
                                                                                                                                                                                                                            FRHTQYPDVPTRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; L06502;
; U03873;
; X59725;
                                                                                                                                                                                                                                                                                                                                                                                         TSSYGHVLERQPALGGRLDSPGNLDTLQAKKNFSVSHLLDLEEAGDMVAAQADESVGEAG
                                                                                                                                                                                                                                                                                  RSLLESPGLTSGSDTPQQD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00027; HOMEOBOX_1; 1.
PS50071; HOMEOBOX_2; 1.
PS50803; OAR; 1.
: DNA-binding; Developmental protein; Nuclear protein; ive splicing; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; AAA39672.1; -.; AAC52139.1; -.; CAA42410.1; -.; AAB46839.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                   -GGNQEPRQQPQPPPEEPAQAAMEGPQPENMQPRTRRTKFTLLQVEELESV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homeobox;
                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; XOH
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235
197
245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                                               -----NDQLNSEEKKKRKQRRNRTTFNSSQLQALERV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 184.5; DB 1
Pred. No. 7.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE PROTEIN BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (POTENTIAL).
SAMATYSATCANNSPAQGINMANSIANLRLKAKEYSLQRNQ
VPTVN -> RSSSLPRCCLHEGLHNGF (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMEOBOX.
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FF867F0D856E1115 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                     408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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COF THE WING BLADE.

OF THE MING BLADE.

IN HAD, THORAX AND ABDOMENT, IN AND IN LATER STACE.

OF THE PROSPECTIVE ANTENNAL AND BROWNER.

OF THE MAXILLARY AND LABIAL SEGMENT PRIMORDIA, AND IN LATER STACES, IN THE ENCORPERSSION IS SEEN FROM STAGE 1 IN THE MANDLEDLAR SEGMENT. IN THE ENTERNAL LATERAL PATCHES. EXPRESSION IN THE INTESTINAL TRACT BEGINS AT STAGE 13, CONTINUES THROUGH STAGES 14 AND 15 IN THE BRODDERM OF THE ANTERIOR IN THE INACTINUES THROUGH STAGES 14 AND 15 IN THE ENDODERM OF THE ANTERIOR IN THE INACTINUES THROUGH STAGES 15 FOUND IN THE DESTRIOR END. EXPRESSION IN THE INACTINUES THROUGH STAGES 14 AND 15 IN THE ENDODERM OF THE ANTERIOR IN THE INACTINUES THROUGH STAGES 15 FOUND IN THE DESTRIOR END. EXPRESSION IN THE PROSPECTIVE THORAX, CLAW ORGAN, ANTENNA, SCUTTELLUM AND WING
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                PROSITE; PS00027; HOMEOBOX_1; PROSITE; PS50071; HOMEOBOX_2; PROSITE; PS50803; OAR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an antitice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resting to the European Bioinformatics institute.
                                                                                                                                                                                                                                                PRINTS; PR00031; HTHREPRESSR. ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                   Pfam; PF00046; homeobox; 1
PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000047; HTH_repressr.InterPro; IPR003654; Homeo_OAR.InterPro; IPR001356; Homeobox.
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-i- SIMILARITY: BELONGS TO THE PAIRED HOMEOBOX FAMILY.

-i- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.

-i- SIMILARITY: CONTAINS 1 OAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genes Dev.
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"Molecular genetics of aristaless, a pin the morphogenesis of proximal and in the morp
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                            SMART; SM00389; HOX;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0000061; al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L08401; AAA28840.1; -
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NCBI_TaxID=7227;
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15-JUL-1999 (Rel. 38, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                     DNA_BIND
                                                                                                            Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P06601;
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                                                                                                               DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7:114-129(1993).
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391
283
360
                                                                                                            Developmental protein;
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                                                         OAR.
  GLN/PRO-RICH
                                                                                   HOMEOBOX.
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distal pattern
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RESULT 15
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Q9H161; Q9H1
16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
SEQUENCE
                                                                                                                                                                                                "Haploinsufficiency of the human homeobox gene ALX4 causes skull ossification defects.";
Nat. Genet. 27:17-18(2001).
                                                                                                                                                                                                                                                                                                        Van Hul W.;
"The ALX4 homeobox gene is mutated in patients with defects of the skull (foramina parietalia permagna, J. Med. Genet. 37:916-920(2000).
                                                                                                                                                                                                                                                  MEDLINE=20578741; PubMed=11137991; Mavrogiannis L.A., Antonopoulou I., Baxo Sugayama S.M., Salamanca A., Wall S.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                     Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.; "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain v
                                                                                                                                            MEDLINE=21245130; PubMed=11347906;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          Sugayama S.M.,
Wilkie A.O.M.;
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MEDLINE=20558895; PubMed=11106354;
                                                                                                                                                                                                                                                                                                                                                                                                                            "Haploinsufficiency of ALX4 as a potential cause of parietal foramina in the 11p11.2 contiguous gene-deletion syndrome."; Am. J. Hum. Genet. 67:1327-1332(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shaffer L.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE-20489877; PubMed-11017806; Wu Y.-Q., Badano J.L., McCaskill C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homeobox protein
ALX4 OR KIAA1788.
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15-JUN-2002 (Rel. 41, Last annotation update)
Homeobox protein aristaless-like 4.
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         DEVELOPMENT.
SUBUNIT: BINDS DNA (BY SIMILARITY).
SUBCELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: EXPRESSION IS LIKELY TO BE
                                                             large Proteins in vitro.";
Res. 8:85-95(2001).
FUNCTION: TRANSCRIPTION FACTOR
 FOUND
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Pred. No. 1.6e-06;
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                                                                INVOLVED
                                                                                                                                                                                                                                                                   Baxova A., Kutilek S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vogel
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permagna, OMIM 168500).";
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PROSITE; PS50803; OAR; 1.
Homeobox; DNA-binding; Developmental
Transcription regulation; Activator;
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EMBL; AF308822; AAK38835.1;
EMBL; AF308823; AAK38835.1;
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-I- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
-I- SIMILARITY: CONTAINS 1 OAR DOMAIN.
-I- CAUTION: REF. 1 SEQUENCE CONTAINS A FRAMESHIFT DUE
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InterPro; IPR001356;
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                                                                                                                                                                                                                                                              DOMAIN
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                                               134
  194
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                        86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERRONEOUS SINGLE-NUCLEOTIDE DELETIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTOCKI-SHAFFER SYNDROME
ASSDLPSPLEKADSESNKGKKRRNTTFTSYQLEELEKVFQKTHYPDVYAREQLAMRTDL
                                             DGSLKLQEGSSGHSAALQVPCYAKESSLGEPELPPDSDTVGMDSSYLSVKEAGVKGPQDR
                                                                    DGGM-IPEGGGGNQEPRQ---
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                        ----PENMQ-----PRTRRTKFTLLQVEELESVFRHTQYPDVPTRRELAENLGV
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AJ279074;
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AF308824;
AF308825;
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an email to license@isb-sib.ch).
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US-08-710-249-3
                                                                                               Sequence 3, Application US/08710249 Patent No. 5858777 GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junii
APPLICANT: Andrews, William H.
APPLICANT: Addms, Robert R.
APPLICANT: Addms, Robert R.
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larity 56.7 Conservative GAACTCGGCGCAC GGTACAGACGCAC ACACTCAATACCC	on US  g Yoo Place Place 729 NUMBE 1998 t 6.1	467 1021 1930 1995 1995 1403765 4325 4327 15378 409 43765 4403765 4425 4425 4425 292
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NO. 4.6e-09; smatches 100; GCTGTTGCAGGTGGAG  CCACTCTCAGCTGCATT  CCACTAGAAGGAACTT	last-specific 9,888B	US-08-712-948-6 US-09-095-117-7 US-08-425-069-3 US-09-103-840A-2 5218895-1 US-09-397-787-191 US-09-319-648-22 US-09-319-648-22 US-09-319-648-22 US-09-103-840A-2 US-09-103-840A-2 US-09-135-994-1
aps 385 547 445 505		Sequence 6, Appli Sequence 7, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Patent No. 5215895 Sequence 191, Appli Sequence 1, Appli Sequence 22, Appli Sequence 50, Appli Sequence 50, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli
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INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 4080 base pair
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REFERENCE/DOCKET NUMBER: 011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                   APPLICANT:
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                  APPLICANT:
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LOCATION:
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STRANDEDNESS: single
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Storella, John R.
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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ches 87;
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; OTHER INFORMATION:
US-09-220-157A-3
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Best Local Similarity
Matches 109; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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611 TCCGGAAGAAGCAGCG
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                                                                                                                                                         375 TGGAAAGTGTTTTCCGACACACTCAATACCCTGATGTGCCCACAAGAAGGGAACTTGCCG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Storella, John R. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                     AAAACTTAGGTGTGACTGAAGACAAAGTGCGGGTTTGGTTTAAGAATAAAAGGGCCAGAT 494
                                GTAGGCGACATCAGAG 510
                                                                  TGTGCACCAACCTGCCTGAGGCCCGGGTGCAGGTGTGGTTCAAGAACCGCCGGGCCAAGT 610
                                                                                                                                     TGGAAAAGACCTTCCAGAAGACTCACTACCCAGATGTGGTGATGCGTGAGAGGCTGGCCA 550
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55.6%;
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2.3e-05;
hes 87;
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RESULT 4 US-08-957-351-6

Sequence 6, Application US/08957351 Patent No. 6306586

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US-08-957-351-5
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Best Local Similarity 52.9%;
Matches 148; Conservative
                Sequence 5, Application US/08957351
Patent No. 6306586
GENERAL INFORMATION:
APPLICANT: Semina, Elena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UII
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: FOLEY, HC
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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   APPLICANT:
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NAME: Arnold, Beth E.
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STRANDEDNESS: single
TOPOLOGY: linear
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Murray,
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Jeffrey C
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Pred. No. 2.1e-05;
0; Mismatches 126;
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US-08-958-642-3
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US-08-957-351-5
                                                                                                                                                                         Sequence 3, Application Patent No. 5948623
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Best Local Similarity
Matches 148; Conserv
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                                                                                                                                                        GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL METHOI TITLE OF INVENTION: DIFFERENTIAN NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/957,351
FILING DATE: 24-OCT 1997
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                      APPLICANT:
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ZIP: 02109-2170
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SYSTEM: PC-DOS/MS-DOS
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                                                                                NOVEL METHOD FOR TESTING THE DIFFERENTIATION STATUS IN PANCREATIC CELLS OF A MAMMAL
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Pred. No. 2.1e-05;
0; Mismatches 126;
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Best Local Similarity
Matches 107; Conserv
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Patent No. 6028184
GENERAL INFORMATION:
APPLICANT:
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                                                                                                                                                                                             CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
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SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                     FEATURE
                                                                    MOLECULE TYPE:
DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "oligonucleotide"
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LOCATION:
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TOPOLOGY: lin
                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: sing
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EDNESS: single
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/desc = "oligonucleotide"
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n Release #1.0, Version #1.30 (EPO)
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Pred. No. 4.7e-05;
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Best Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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DESCRIPTION:
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LENGTH: 2481 base pair
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                                499 GCGACATCAGAGA 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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AAGAGAAGAAA 1014
                                                                                                      CTTAGGTGTGACTGAAGACAAAGTGCGGGTTTGGTTTAAGAATAAAAGGGCCAGATGTAG 498
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IBM PC compatible
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/desc = "oligonucleotide"
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Pred. No. 4.7e-05;
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Pred. No. 4.7e-05;
0; Mismatches 86;
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US-08-957-351-2
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US-08-957-351-2
           Sequence 1, Application US/08957351 Patent No. 6306586 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Semina
APPLICANT: Murray
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TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Arnold, Beth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
APPLICANT:
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REFERENCE/DOCKET NUMBER: UIA-024.01
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One Post Office Square
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VENTION: METHODS AND COMPOSITIONS FOR THE
VENTION: DIAGNOSIS AND TREATMENT OF CATARACTS
Semina,
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 5.8e-05;
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                   CURRENT APPLICATION NUMBER: US/09/636,735A
CURRENT FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1251
TYPE: DNA
                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local Similarity 56.4%;
Matches 102; Conservative
                                                                                                                                                                                                                        Sequence 1, Applic Patent No. 6416956
                                                                                                                                              APPLICANT: Berg, Patricia TITLE OF INVENTION: No. 64169 FILE REFERENCE: 179.37405X00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0.
FILING DATE: 24-OCT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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METHODS AND COMPOSITIONS FOR THE
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                                                                                                                                                                 6416956el Transcription Factor,
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US-08-958-642-1
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                                                                                                                              Query Match
Best Local
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Best Local Similarity 51.3%;
Matches 121; Conservative
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FILING DATE: December
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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LOCATION: (633)..(812)
OTHER INFORMATION: homeobox
NAME/KEY: CDS
LOCATION: (285)..(1004)
                                                                                                                                                                                                                                        TOPOLOGY: 1i
MOLECULE TYPE:
DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                401
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                                                                             341 CGCACGAAGTTCACGCTGTTGCAGGTGGAGGAGCTGGAAAGTGTTTTCCGACACACTCAA 400
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                                                                                                                                                                                                                                                                                                        TYPE:
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TACCCTGATGTGCCCACAAGAAGGGAAACTTGCCGAAAACTTAGGTGTGACTGAAGACAAA 460
                                               CGGGCTATCTTCTCCCCGGGACAAGCCGAGGCACTGGAGAAAGAGTTTCAGCGTGGGCAG 744
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                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                   nucleic acid
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                                                                                                                                                                                                                                                                                                                  1275 base pairs
                                                                                                             Conservative
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SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0,
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DIFFERENTIATION STATUS I
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er 31, 1996
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ches 115;
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                                                 Sequence 1, Application Patent No. 6071697 GENERAL INFORMATION: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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TITLE OF INVENTION: DI
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
.LENGTH: 1275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palanaming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           745 TATCCAGATTCAGTGGCCCGTGGGAAGCTGGCTGCCGCCACCTCTCTGCCTGAAGACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCGCCAATGAACTACGTGCTGACCCAGAC
                                                                                                                                                                                                        CTCGCCAATGAACTACGTGCTGACCCAGAC
                                                                                                                                                                                                                                                                                                                                                                                     CGGGCTATCTTCTCCCCGGGACAAGCCGAGGCACTGGAGAAAGAGTTTCAGCGTGGGCAG 744
                                                                                                                                                                                                                                                      GTGAGGGTTTGGTTTTCTAACAGAAGAGCCAAATGGCGCAGGCAAGAGAAGCTGAAATGG
                                                                                                                                                                                                                                                                                   GTGCGGGTTTGGTTTAAGAATAAAAGGGCCAGATGTAGGCGACATCAGAGAGAATTAATG
                                                                                                                                                                                                                                                                                                                      TATCCAGATTCAGTGGCCCGTGGGAAGCTGGCTGCCGACCTCTCTGCCTGAAGACACG 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Application 6028184
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166..1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /desc = "oligonucl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.9%;
   NOVEL METHOD FOR TESTING THE DIFFERENTIATION STATUS IN PA
                                                                                                   US/08778423A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51.6; DB 3;
Pred. No. 0.00035;
0; Mismatches 99;
                                                                                                                                                                                       894
                                                                                                                                                                                                                    550
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   PANCREATIC CELLS
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; LOCATION:
US-08-778-423A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-590-894C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic ac.
DESCRIPTION: /desc = "polingment"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/07590894C Patent No. 5342761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.9%;
Best Local Similarity 52.9%;
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5237
                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/590,894C
FILING DATE: 01-OCT-1990
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           865 GAAGCACAGCTGCCAGGTGCTTCCCAGGAC 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521 CTCGCCAATGAACTACGTGCTGACCCAGAC 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 TACCCTGATGTGCCCACAAGAAGGGAACTTGCCGAAAACTTAGGTGTGACTGAAGACAAA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 CGCACGAAGTTCACGCTGTTGCAGGTGGAAGGAGCTGGAAAGTGTTTTCCGACACACTCAA 400
                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 77010-3095
                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                    CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/778,423A FILING DATE: December 31, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGAGGGTTTGGTTTTCTAACAGAAGAGCCAAATGGCGCAAGGAGAAGAGAAACCTGAAATGG
                                                                                                                                                                                                                                                                                                                       E: Dr. Benjamin A. Adler
1301 McKinney St. 41st Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                     MacLeod,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other nucleic acid
/desc = "oligonucleotide"
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A No. 5342761el Onco-Fetal Gene, Gene Product
and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51.6; DB 3;
Pred. No. 0.00035;
0; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99;
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Search completed: April 28, 2003, 19:25:28 Job time: 72 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                      8.4%;
Best Local Similarity 49.8%;
Matches 150; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                     .556 T 556
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                                                                                                                                                                                                                                                               376
                                                                                                                                                                                                                                                                                                   426 TGGGGGTAGGCAGATGCCCCTCCAGGGCTCTAGGTTCGCCCAGCATCGACTGAGGGAACT
663 T 663
                                                                          603 CAGAAGAAACAGGAGGAGGGCAACACCAGTCCCTGAACATTTTAGAGGAACATTCGAGTG 662
                                                                                                                                                                                                                                                                                                                                      316 CGAGAACATGCAGCCACGAACTCGGCGCACGAAGTTCACGCTGTTGCAGGTGGAGGAGCT 375
                                                                                                                                                                                                                                                                                                                                                                           366 GGAGCAGGAACAAAATGAGCCAGTTGCTGAGGGCACTGAGAGCCAGGAGAATGGAAATCC 425
                                                                                                                                                                                                                                                                                                                                                                                                              CELL TYPE: T-cell
CELL LINE: SL12.4 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: SL12 cell line DEVELOPMENTAL STAGE: Bone marrow-active Type: Lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 713-651-5587
TELEFAX: 713-651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN: AKR1 Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                           TAGGCGACATCAGAGAGAATTAATGCTCGCCAATGAACTACGTGCTGACCCAGACGACTG 555
                                                                                                                                                                        AAACTTAGGTGTGACTGAAGACAAAGTGCGGGTTTGGTTTAAGAATAAAAGGGCCAGATG 495
                                                                                                                                                                                                                          GGAGTCCATTTTGCAGCGCACTAATTCCTTTGATGT---CCCAAGGGAGGATCTTGATAG 542
                                                                                                                                                  ACTGATGGATGCCTGTGTGTCCAGAGTGCAGAATTGGTTTAAGATCAGGAGGGCTGCGGC 602
                                                                                                                                                                                                                                                             GGAAAGTGTTTTCCGACACACTCAATACCCTGATGTGCCCAACAAGAAGGGAACTTGCCGA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         838 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA to mRNA
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